



Docket No.: CL001188

Serial No.: 09/817,198

Inventors: YE, Jane et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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1 TGCCCGCTGC CCGCCCGCAG TTCCCCGCC CGCTGGCCCC AGTCATGGCG
51 AAGCACTACG ATGTGCTGTT CCGGCTGCTG CTGATCGGGG ACTCCGGGGT
101 GGGCAAGACC TGCCTGCTGT GCCGCTTCAC CGACAACGAG TTCCACTCCT
151 CGCACATCTC CACCATCGGT GTTGACTTTA AGATGAAGAC CATAGAGGTA
201 GACGGCATCA AAGTGCAGGAT ACAGATCTGG GACACTGCAG GGCAGGAGAG
251 ATACCAGACC ATCACAAAGC AGTACTATCG GCGGGCCCAG GGGATATTT
301 TGGTCTATGA CATTAGCAGC GAGCGCTCTT ACCAGCACAT CATGAAGTGG
351 GTCAGTGACG TGGATGAGTA CGCACCAAGA GGCCTCCAGA AGATCCTTAT
401 TGGGAATAAG GCTGATGAGG AGCAGAAAAGC GCAGGGTGGGA AGAGAGCAAG
451 GGCAGCAGCT GGCAGAAGGAG TATGGCATGG ACTTCTATGA AACAAAGTGCC
501 TGCACCAACC TCAACATTAA AGAGTCATTC ACCGCCTCTGA CAGAGCTGGT
551 GCTGCAGGCC CATAGGAAGG AGCTGGAAGG CCTCCGGATG CGTGCCAGCA
601 ATGAGTTGGC ACTGGCAGAG CTGGAGGAGG AGGAGGGCAA ACCCGAGGGC
651 CCAGCGAACT CTTCGAAAC CTGCTGGTGC TGAGTCCTGT GTGGGGCACC
701 CCACACGACA CCCCTCTTCC CTCAGGAGGC CCGTGGGCAG ACAGGGGAGC
751 CGGGGCTTTG CCCTGCTGCT GTCCCTCTCGT GTGATGACCC TATTGAGTAT
801 CAGTAGCCAC TACTCCCCCT GCCTGGCCCT GAGAGCGGCT CTGCTGTCAT
851 CTCAGCAGC CCCTGTCCCC AGCCCCGTCGA CCCTGGAGTG GTCTTCTTCA
901 GCCTGTTTCC CCAGCACAG GCCTGCTACG ACCCCCCACGA TGTGCCGCAA
951 GCACTGTCTC ACCATCCCCG ACCCACCCAGA CAACAGCCAG GGCTGGAGTC
1001 CAGGCCACTT TCAGCTGCTC CTTTCTCCGT GCATCGTGT CTTCTCTGC
1051 TTTTCTCTC TTCCCCCCTC TCTCTTCTC TGACCCCTCC CCTCCGGTGC
1101 GTTTCGTATC AAAGCTCCTC AAACCCCGTC CCCCCTGTGT CCTGCTGTGT
1151 GCAGCTCGCT CTTTCTCTTC TTCTCTAACGT ATCCAAGGGG ATGGACCCAG
1201 GCTCGTGGGG AGGTTCCACC CTTGGATCCA GGAAGAACCC TCCACCTGC
1251 CTCGTGGGTG GGCCAAAGGC TACAGGGTGC TTCTCTCTC TCCCCCACCC
1301 CCACTGTCCC TCATGTGCCA TGGGCTTGCC TCCCCAGTGA CCTGCGAAAG
1351 TGGAGCATCG AGGTAGGAGG GAAACAGCAA CCGGGGAGTC CTCGAGCTG
1401 GGGCTGCCCT ACCTCTACCC ATTCCCCGAC CAGAGCTTTG CCCTTGCTTG
1451 GCTGCCGCC TGCCTCTTGG GGGAACTGAG CTCAGAGGCA GGTGCTTCAG
1501 AGAAGGAAAC AAAATGAGGG GTGGCAGGG AAAAAAGTCA CCTCCATTCT
1551 CTACCTCCA TGCAGCATGA ACACAATTTC TCTCCACCTG GCTCCAAAT
1601 TTAAGAGATGT GGACCAAGGC CTGTGGGTAC TCCAGGGCA AGGAGAGCCC
1651 TGGGGTCAGT GACACTGTCA GGCCAAACCAT GCACCTCCACA AAGGGGAGCA
1701 TTTGAAATG AAGGACTAGC TCCTATGTAT CAGGTTAAGA GCAAGGGAGA
1751 GCTGCCAGG GACAGCAGTT TGACACAGCAG AGGGGAATGT AGCAACAGCA
1801 GGGCCTCTA GGCCCCATCT TCCATTCTT AGGTAAGAAG AGCATTCTC
1851 CAGACTCCC GGCGGAGGAC TGAGCTAGC CTTCAGCAAC CAAGGTTCTC
1901 CTGGGACCCA AAGTTTATGG GAGAAGGGCA AAGACTTCAT GGGAAAGAG
1951 AAGGAAGGCC CTGGGTAGAA ACGCTTGGTG CTGTTCTCTT TGGCCTTAA
2001 GACAAAGCGC TCATCTTGCC CTCTACCTCC TGATAGGCTT GAGGGTTTGC
2051 CAACCACACT GTGGCTACAG GTGGAGGGAA GAGGACTCCT TCCTCCAGAG
2101 TGCTATGTT AGGAAGTTTC TTTAACCCCA TATGGCCCAA GAGTAGCTCG
2151 TAGGAGGCC TTTAAAGACG GAACAAGTAA TTTACCAGTT CTACTGGGT
2201 TCCTGCCAC CGTCCCAAGG TGGGCCAGGC CTAGGAAGAG GGTCTATTCTT
2251 AAGCCACACA TTAGCTGCAC TGCCTGGCTG CAGCCAAAAC AAAGAACTGG
2301 GTGTGAGTA TTCATCAACT AAGAACCAAAT CTCAGGGCA CTCATATGTG
2351 AAGGATAAGA ACCTCACTTC CTTACTCCTC CAAAAGAAG TGGGGAAAGA
2401 ACCATCAAAC CTTTCTCTCC GACTTACCAA ACCAGGAAAA CAGCAGGAGA
2451 GGGTGGCTA GGACTTAGGG ACAGGGTATA GCTTAGATGG TGGAAAGCAA
2501 AGGAGAGCAG GAAGTTGTAATC ACTACTGGCT AATGAGAAAA GGAGACAGCT
2551 AACTCTAGGA TGAAGCTGTG ACTAGGCTGG AGTTGCTTCC TTGAAGATGG
2601 GACTCCTTGG GTATCAAGAC CTATGCCACA TCACACTGGG GCTAGGGAAAG
2651 TAGGTGATGC CAGCCCTCAA GTCTGTCTTC AGCCAGGGAC TTGAGAAAGTT
2701 ATATTGGCA GTGGCTCCAA TCTGTGGACC AGTATTTCAAG CTTTCCCTGA
2751 AGATCAGGCA GGGTGCCATT CATTGTCTT CTCTCCTAGC CCCCTCAGGA
2801 AAGAAGGACT ATATTTGTAC TGTCACCTAG GGGTTCTGGA AGGGAAAACA
2851 TGGAAATCAGG ATTCTATAGA CTGATAGGCC CTATCCACAA GGGCCATGAC
2901 TGGGAAAGG TATGGGAGCA GAAGGAGAAAT TGGGATTTA GGGTGCAGCT
2951 ACGCTCACCC TAAACTTTG GTGGCCTGGG GCATGTCTG AGGCCAGAC

FIGURE 1A



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3001 TGTTAACGAG GCTCTGCTGG CCTGTTACT CGTCACCAAC TCTGCACCTG
3051 CTGTCTTGAG ACTCCATCCA GCCCCAGGCA CGCCCACCTGC TCCTGAGCCT
3101 CCACTATCTC CCTGTGACGG GTGAACCTCG TGTACTGTGT CTCGGGTCCA
3151 TATATGAATT GTGAGCAGGG TTCATCTATT TTAAACACAG ATGTTACAA
3201 AATAAAGATT ATTTCAAACC ACCAAAAAAA AAAAAAAA AAAAAAAA
3251 AAAAAAA (SEQ ID NO:1)

FEATURES:

5'UTR: 1-44
Start Codon: 45
Stop Codon: 681
3'UTR: 684

Homologous proteins:

Top 10 BLAST Hits

		Score	E
CRA	335001101587561 /WO200058473 /org=Homo sapiens /taxon=9...	428	e-119
CRA	18000004937398 /altid=gi 464561 /def=sp P35289 RB15_RAT RAS...	423	e-117
CRA	18000005187045 /altid=gi 7498104 /def=pir T33855 hypothetical...	220	6e-56
CRA	18000004929618 /altid=gi 131798 /def=sp P24407 RAB8_HUMAN R...	216	1e-54
CRA	335001098683352 /altid=gi 11422744 /def=ref XP_001482.1 TR...	214	4e-54
CRA	18000005096141 /altid=gi 2317272 /def=dbj BAA21744.1 (AB00...	214	4e-54
CRA	18000004952869 /altid=gi 131848 /def=sp P22128 RAB8_DISOM R...	212	3e-53
CRA	335001098688905 /altid=gi 11432830 /def=ref XP_007682.1 RA...	211	4e-53
CRA	18000004945380 /altid=gi 131847 /def=sp P22127 RAO1_DISOM R...	211	5e-53
CRA	18000005163099 /altid=gi 7705849 /def=ref NP_057215.1 ras...	210	6e-53

BLAST dbEST hits:

		Score	E
gi	12333507 /dataset=dbest /taxon=96...	626	e-177
gi	12120217 /dataset=dbest /taxon=96...	377	e-102

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|12333507 brain

gi|12120217 epid_tumor

From tissue screening panels:

Fetal whole brain

FIGURE 1B



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1 MAKQYDVLFR LLLIGDSGVG KTCLLCRFTD NEFHSSHIST IGVDFKMKTI
51 EVDGIKVRIQ IWDTAGQERY QTITKQYYRR AQGIFLVYDI SSERSYQHIM
101 KWVSDVDEYA PEGVQKILIG NKADEEQKRQ VGREQQQLA KEYGMDFYET
151 SACTNLNIKE SFTRLTELVL QAHRKELEGL RMRASNELAL AELEEEEGKP
201 EGPANSSKTC WC (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

205-208 NSSK (SEQ ID NO:6)

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 2

1 92-94 SER
2 206-208 SSK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 2

1 29-32 TDNE (SEQ ID NO:7)
2 104-107 SDVD (SEQ ID NO:8)

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

101-109 KWVSDVDEY (SEQ ID NO:9)

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 2

1 18-23 GVGKTC (SEQ ID NO:10)
2 136-141 GQQLAK (SEQ ID NO:11)

[6] PDOC00017 PS00017 ATP_GTP_A
ATP/GTP-binding site motif A (P-loop)

15-22 GDSVGKG (SEQ ID NO:12)

[7] PDOC00579 PS00675 SIGMA54_INTERACT_1
Sigma-54 interaction domain ATP-binding region A signature

11-24 LLLIGDSGVGKTCL (SEQ ID NO:13)

FIGURE 2A



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BLAST Alignment to Top Hit:

>CRA|18000004937398 /altid=gi|464561 /def=sp|P35289|RB15_RAT
RAS-RELATED PROTEIN RAB-15 /dataset=nraa /length=212
Length = 212

Score = 423 bits (1077), Expect = e-117
Identities = 207/212 (97%), Positives = 209/212 (97%)
Frame = +3

Query: 45 MAKQYDVLFRLLLIGDSVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 224
MAKQYDVLFRLLLIGDSVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
Sbjct: 1 MAKQYDVLFRLLLIGDSVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60

Query: 225 IWDTAGQERYQTITKQYYRRAQGIFLVLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 404
IWDTAGQERYQTITKQYYRRAQGIFLVLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120

Query: 405 NKADEEQKRQVGREQQQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 584
NKADEEQKRQVGREQQQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKEL+GL
Sbjct: 121 NKADEEQKRQVGREQQQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELDGL 180

Query: 585 RMRASNELALAELEEEEGKPEGPANSSKTCWC 680 (SEQ ID NO:2)
R ASNELALAELEE+EGK EG PANSSKTCWC
Sbjct: 181 RTCASNELALAELEEDEGKTEGPANSSKTCWC 212 (SEQ ID NO:4)

>CRA|335001101587561 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
/mol_type=protein /date=08-FEB-01 /length=218
/altid=derwent_id|B41604 /altid=derwent_ac|B41604
/def=Human ORF1368 polypeptide sequence SEQ ID
NO:2736 /patent=WO200058473-A2 /pat_section=Claim
Length = 218

Score = 428 bits (1088), Expect = e-119
Identities = 212/218 (97%), Positives = 212/218 (97%), Gaps = 6/218 (2%)
Frame = +3

Query: 45 MAKQYDVLFRLLLIGDSVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 224
MAKQYDVLFRLLLIGDSVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
Sbjct: 1 MAKQYDVLFRLLLIGDSVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60

Query: 225 IWDTAGQERYQTITKQYYRRAQGIFLVLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 404
IWDTAGQERYQTITKQYYRRAQGIFLVLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120

Query: 405 NKADEEQKRQVGREQQO-----QLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHR 566
NKADEEQKRQVGREQQQ QLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHR
Sbjct: 121 NKADEEQKRQVGREQQQKCPSLQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHR 180

Query: 567 KELEGLRMASNELALAELEEEEGKPEGPANSSKTCWC 680 (SEQ ID NO:2)
KELEGLRMASNELALAELEEEEGKPEGPANSSKTCWC
Sbjct: 181 KELEGLRMASNELALAELEEEEGKPEGPANSSKTCWC 218 (SEQ ID NO:5)

FIGURE 2B



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Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00071	Ras family	323.8	8.2e-95	1
CE00060	CE00060 rab_ras_like	211.0	1.8e-59	1
PF00006	ATP synthase alpha/beta family	4.2	2.1	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00006	1/1	10	24 ..	203	217 ..	4.2	2.1
CE00060	1/1	2	165 ..	16	184 ..	211.0	1.8e-59
PF00071	1/1	10	212 .]	1	198 []	323.8	8.2e-95

FIGURE 2C



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1 GCTCAAGATT GCACAGCTGG TGAGTGGTGA CACTGGGACT GGAACCCAAG
51 TGTGCCCTAAC TCCAGAGCCC TTGGCATGCA CCTGAAACCC CATGTAAGCC
101 CACTGTGGAG ACGCGCACCT CGAAATAATG GAATCCACTA CATCAGTCC
151 TTTAGCTTTC TGTGTAATCA GAGTAGCTAG CAGGCTCGGG ATTCGCCCC
201 CCGGCTTTT TTTTTTTTTT TTTTGAGAC AGAGTTTGC TCTTGTGCC
251 CAGGCTGGAG TGCAATGGCG CAATCTCGC TCACCGAAC CTTCGCCTCT
301 CAGGTTCAAG CAATTCTCCT GCCTCAGCCT CCCGAGTAGC TGGGATTACA
351 GGCACCGGCC ACCACGCCA GCTAATTTTT TTATATTTT AGTAGAGATG
401 GGGTTTCACC ATGTTGGCCA GGCTGGCTT GAACCTTTCC CCTCTTATTA
451 TAATTCAAGAC ACTTAACCTG AAATATACCT TTTCAAATGA AGTAAATGGG
501 CTTACCACTT CCCTTGACCT ACTATTGAAA AATACATTCT CCATCCAATA
551 TTCAGCCTGA AACACAGGTAT GTACATATAT ACTTTTCATT GCTTTTTTT
601 TTTTTTTTTT GAGACAAGGT CTCCCTCTGT TGCGCAGGCT GGAGTGCAGT
651 GTCATGATCT CGGCTCACTG CAGCCTCCCC CTAATGGGTT CAAGCAATCC
701 TCCCACCTCA GCCTCTCAAG CCTGGGATTA CAGGCGAGCC ACCGTGCCA
751 GCTAATTTTT TTATATTTT AGTAGAGACT GGTTTCACT ACATTGGCA
801 GGCTGGTCTC CAGCTCTGA CCTCAAAGTG ATCTGCCGC CTCAGCCTCC
851 CAAAGTACTG GGATTACAGG CATGAGCCAA CGCGCCTAGC CTTTCATTGC
901 TTTTAAAGA CTTAATAGGC TAGACTTTGC TCTCCCTCAA TACTCGTTGG
951 TAGGGATAGG CAATTTCTC AACTCCGGAG AGCATTCTT TGCCCTCTC
1001 CGGTGCTAAC ACATTCACTG GTAGGAAACT GGATCTTGA CAAGGGCCAT
1051 TCATTCTTG GTGCCACTGG CTATACCACA GAGAAATTAA GGGGTCTGAA
1101 ACAATACATT GGTCAACCTGG GCACCTATCC TAAGCACCTT AGAGGGAAA
1151 CGGAGACTTG CCCGCACACC TCTAAAGGAT TTGCACTTG GAGATGTTCT
1201 TATGCCATC TATCTTTCA CCCTGGTGA GGCGGTGAAT AGGCATTTC
1251 CCCATTAAA GAAAAAAATGG GGACGGGGGA GGGCGTGAC ACAGTCACAC
1301 AGGTAAAGGGG CAGCCAGATG GCAGGGAGGG GGAATTCCAC CCACACTCTC
1351 GGGGACTCAT GGAGACGGGT GTTCAATCC AGATCCTGCT CAAGGCCCTC
1401 CTACCTGGG TGAGCCCAGC TGAGGTACCA GCCACTGGGG AGCCGGGCCA
1451 GATCCTGCAG ATGCAGGGTG CCACGGCGG CGGAATTACC GGCGCCAGAC
1501 TTGGGGTGGG ATATGGGGAG AAGTGGTGAG CCCGGAAAGC GGAGCACGGT
1551 AGAAGTGGGC TGGGTGGGG CTCACCTCAA CTCCCCCATT CGGAGCGTCC
1601 GCGGAAAAAC GAAAACGTTT CCCCCGCCCG GGAGGAAGG GGTTGGGAGG
1651 GGGGGCTGGC GCCCCGCCCC AGCGTCGCT GCTCGATGGG GTCCCGCTCT
1701 CCTGCGCGCG CTCCCCGCC CCTCTCTACC GGGGCGGCGG CGGCGGCCGA
1751 GGGGAAGGGG CGGGCAGGGG CGGCCGCCGG TTTCCTCTCC CACCGCCTCG
1801 CGCCAGCCA GCGAGCCGA GCGAGCCGA GCGGGCGCCG CGCCGGGCTC
1851 CCGCCGCGC CGCGCTTCCC GGCACCCAGC GAGCGAGTGG GCAGGGGGC
1901 GGGCGAGGCA GCGCGGGGG CGGGGCCCG CGTCCCTCTC GCGGCCCGCA
1951 GCGTCCCCGG CGGGGCGCGG GCGCGATGG CAGGGCGGA GCAGGGCTGA
2001 GCCCGCTGCC CGCCCGCAGT TCCCGGCCCC GTGGGCCCCA GTCATGGCGA
2051 AGCAAGTACGA TGTGCTGTT CCGCTGCTGC TGATGGGGA CTCCGGGGTG
2101 GGCAGAACCT GCCTGCTGT CCGCTTCACC GACAACGAGT TCCACTCTC
2151 GCACATCTCC ACCATCGGTG AGGGGGGTG GCGGGGGCG CCCCCTCTC
2201 CCCGCCCGG GCCCCCTTCC CCGGCCGCCCC CGTCCCCAGC TGGGGAGGAA
2251 TTGCGCAGCCC CTCCGGCTGG AGGCAGGGC GCGGGAGGCC GGAGTCCGGG
2301 ATAAATCTCG GGGTGAGCAT AGGTTTGGC AGGTGAGGGT GTCCCTGCTG
2351 CCTGCCGTCC GGACCAAGGGG TGGGGTCTCC CGCCTCTTGC CGGGAAGCCT
2401 TCCGTCCCCAT CAAACCGAGA AACCGGGGGT GAGGGGAGCT GGTGTAGGCC
2451 TGGGTACCCC GAGCTGGGGT AGCAAGAAC TGAGCCGCTG GAATAAACACC
2501 CCCACACCCC CAGGGGGAGG GGAAGTAAAG CTTCTGCTAC GGAAAAGGGG
2551 GTCAGGGTGG AGACCGGGAGT CACTGAGGCG CCGTTGGTTC TGTGGTGACC
2601 CAAGGTGGAG CGGGCGGGGG GCGAGGGGG GAAGAGAGGA CGTACGGAGG
2651 GGCCACAGGG ATCGAGTTTC CAGGGCAGAG TTGGGAAGGT AAGCCGCAAG
2701 GTGGGACACC TGGGGGAGGA CACAGATAGG GTGAGGGAGCC CCTGCGCCTG
2751 GGAAGAGGGAG ACATCTGTT TGAGGGAGGC TAAAGAGGGAT GGAGGAGTGT
2801 CAGGAATACC TGCCCAGACC AAGGGTCAG AAGGCAGGCA GGACCCGCC
2851 GAGGGCATCT CTCATCTGGC AGTGCTGGAG CCTGTGGTTA GAGGGACAAG
2901 ACCCGGTGGC ATCCCAGACA GCACTATGAT GGGGTCACTT ATTCTAGGAA
2951 TGGGTCCATG GCCTCCCCCTC TGAGACAGTC AGTCTCCCGC TTCTAGGCTG

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FIGURE 3A

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3001 TGAGGGGCC CCTCCCTGAG AAGTCTGAGT AGAGGGAATT TCATCCTCAG
3051 CTGCTACCCG GGTCAAGCCCT GGAGTAGCCT CTGCATTGCC CAAGCCCCCTG
3101 GAAACACCTG CTGGCTGGCT GGTCACTCCAT TTGGAATGCT CTCCTAGAAG
3151 TCCCTGCTGC CATCAGGGAT GGGCACCCAGC TCTCAGCTTC CTCTTGAGGA
3201 TTCATGTCCA CACCATCCCC CCTCCCCCCC ACACACATTC CTTGCTGAGA
3251 GAGAAGTAGG AGCAGATAGA TACAGCCAGG AGGAACAGAA CCTTCTGGTT
3301 AAGAAGCCAG CTTTATTGTC CAAGAGACCT GAGACCTCAC TGTGGGGCAA
3351 AGCAACCTG ATATTCGCT AAACCTCTGA GCTTTATTTA GTTTCATC
3401 TGTAGAACGG GTATAATAAT TGCACTTAC TGCAAGTTG TTGTCAAGAT
3451 TAAATGAGAT AACGATTGTT AAGTGTAGG CACAGCCAGA CACATGGTA
3501 AGCTCGATAA ATGCTGATTG TTCTTACTGC TATTGCCATT ATCATTGAGC
3551 TTTTAGGGTC TCCTCTCTT GTTTCACCAA CTTGAAGGGT GAAACAACAG
3601 GACTTAGGGT CAGGGAAACAG AACTTGTCCG TCTTTCTCAG AGGAGCTGTA
3651 AGGCCAACTC TTAGGAAACC CAGGAGCTTG GGCTGAGCCA TGGTTTGGAT
3701 GAGAGACATT GCAGAAAGAA GGGGAGCCTA TAGACACTAA GGCTTTGTGC
3751 CTGCCGGGAG GACTTGGGAG AGAGCCAGGT GCAGGAGAAA GGCAATGGGG
3801 TGATGGAGGA AGTGGCAGAG GAACCAAGATG GTGTATGAGG ACAGGTTGTG
3851 GGCTCAGGGG CAAAGGGCGG TGGGTTATCC CTTAAGGAAA CTAGGAGTGG
3901 CTATTTTGG GAGAGGCCCTG GTGCTTGGAA CTACTGAGCT ATCTCCAGAG
3951 AGCTGTGGGC TGGCTGGGAG GCCCTGGCTT TGGCCTGAAG AGCTGTTGTT
4001 TGACACTGCT CTCCTAGTCC CATTCCAAGT CCTATAGGTG ACATGGACTT
4051 TTCCCTTGA GGGCTTCATT CAACCACTC ATTTCAGAAG CTCTGGGACT
4101 CCTGCTTAGT GCTGTGGGAG GCAGCCCTCC CTGGGAGACA CATAACCTCC
4151 TTTTGAGGG CACCCCTCTT TCTAAAATAC CAGGATGGCC CTCTGAGGCT
4201 CGTGCCTCTCC TAAAGAGAG TCCATTGCCT CACACCTCTA ATCATCCACC
4251 CTTCTCCTTG TCCCTCCCCC TTGTAACTCTC CTTTCTTCTAGA CACCTCTG
4301 TAATAGGTGA ACACTAAATA GGTCACAGGG ACTTCTGTAA ACCCTCCAGG
4351 GCAGACCACT TTGGGCACAT AGGTGAATCA GTGAACGTAG TGGGGTGT
4401 TCTGCAGCAC TGTCTCCCT CAAGGCCCTT GGTATATTGG CCTAAAACCT
4451 AAAGATGGCT CCCAGATTTC TTCCCTCGCT TCTGACACCC GGGTCCCT
4501 TTCTACAGGA CACAGAGGAT TCTCTAGGT CCCCTTTCC ACAGGACACA
4551 GAGGACTCTA GGAGTTGGG TTCCATGGAA TAGAAAGAAA CCTGTCTTC
4601 TTCACACCAG CTTTTAAAAA TCTGCCAAC TGGGTATCTT AAATGTTTC
4651 TTATTTAAAG CTTATTAAGG GACTTGGAT TCTCCCTTAT CTTGGGCGTG
4701 TTTTCAGCA TTAACTAAAAA CTTAAAGGAA AGAGTTGGAT GGTCAAGAAA
4751 AGCTTTTCC TTAAGTGATA TGGACAGTTT CTCAAGGAGG TAGAAGGGC
4801 AGCCAGGAGA CAAATCAAGG AGCCAACGAA ATGAGTGCTA CCAAGTCATA
4851 GTCATTCGCT TATTTTTAAA AAATGCGTGT CCTGTATGCC AGGCTCTGCA
4901 CTGAGACCGA GAGATTCCAA GATGAATAAT ACCTACAGTC ACTGTTCTCA
4951 AATTGTGCAT TACCTAAAAC ACATTACATG ACCATGCTGG CCACTGATCG
5001 AGGCACCTTT CCCAGGGCT TTTTTGTGA ATTAAGAAAA CAAGGTAATT
5051 CACCAAGTTAT TGCCAAGATA GTTGGCTTC TTGGCTCATG TGGATATC
5101 CTAGGCCAGT ACTTTTGTGA TTTACTGTGT ACTCCACTTT AACGGCC
5151 GATCTCTAG AGAAGAACCC GCCAGGGAGC AGTGAGAGGC CTCCCTGGTA
5201 GACTGAGACA CTGACTGTCC CTCCCCCTAT CCTTTCTGTC TTTCTGGCCA
5251 GCAGACCCAGC AGGTGGCCCT GCCACTGGCT CTGCCACAGG CATT
5301 CTGTCAGCT GTGCTGGCCCT GGCTGGGGGT TGGTGCAGG GGGTCC
5351 AATACTACCT TAAACAAATT AATTGAGCAT TCACTACCAA GCTCTGTGCC
5401 AGGCATTTA GAGACATATT GCAGTCTACG TTTTCTGCC ACAGAAGCCC
5451 ATAACCTAGA TGGGGAGGCA AGACAAAGGG AAAAACAAAA AACAAAGAGC
5501 TAGGCCAAA ATGAGATATC TGAAAGAACT TGGTGAATCA CTCTTCA
5551 GTAAAGGATG GATTATGATC ATTGCACTTA CTCTTAATGA AGGTCTCACA
5601 GTGGGTATCA GAAGCTAAAT TATGATGCAA GATGTACCAT GAGGCAGCC
5651 GAGAATGGCG ATGGATGGGA TGGGTGAGTG CTATTCCCAC GACTCC
5701 TGTGGAGGC TGGGGAAAGAG AGAGGCCCT GTGGACTAGA ACCGGCAGGG
5751 AAGGCTGAAG CTAGGCCCTCA GTGTGGCTG CTCGTCAGTT CCTGCAGCAG
5801 AAGGGAGCAG ATGGAGTAAC ATGAGCAGAG ATAACAGAGG TGGGATTGAG
5851 TAGGTGTCCG TGGGGCTCTA GGCAGTTAG ATGCAACAGA AGGGATTCTT
5901 CAGGAAAGTG AGAAGATTCT TCTGTTCTC TCTCTGTCTC CCAAATTATA
5951 AGTGCCTTGA TGGTGCAGACC AAATCTTATT CCTCATTGTT TTTATAGTCC

FIGURE 3B



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Inventors: YE, Jane et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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6001 CTAGTACAGG GCCAGGCAGA TTCAATGCCT GTTGTAAAT TAATGAATGA
6051 ATGCAGGGAC CAGTGGCAG AGGGCATTGA GAGCCTGGCC AAGGAGGTGG
6101 AACATGAGCC TTAGCAATGG TAGGAGGGGT TTTGAGTAGG GTACTAATGA
6151 GGTTGGCTGG AAAGAAGGGGT TAAGACTTGA AGCAGGGAGA CTAGTCAGGG
6201 GCTGCAGTAG TATCCTGGGC ATGAAGGAAC CTCTGAATGG CCCCTCACCC
6251 CCAGTGGTAC CAACACCAAC TTCCACACAG TCAGTTGTTT TACTTTCCCT
6301 CCAGAATGGG GAGTGGTCA AGCCAATCAA CCTGGCAACT TCTGAAAGAA
6351 TCTTATGGGA CCTGTGCCAT GACCAGGTAG GGAGAAGATG TCATACATGG
6401 ACATCTATGT TCAGGGGACC TTTGAGGACC TTTCTGCATG GTGGCCAGGA
6451 GTGAGATGAT GTAAACCACA AATGGAAACT GAAGAGACTG CTCAGGAGTT
6501 GTTGGTTTTC TTTTCTTTTC TATTTTTTTT TTTTGAGAC TAGGTTTCAC
6551 TCTGTCACCC AGTCTGGAGT GTGGTGGTGG CACAATCACG GCTCACTGCA
6601 GCCTCGATCT CCTAAACGCA ATCCCTCCAC CTCAGCCTCT CAAGTAGCTG
6651 GGACTACAGG TGCATGCCAC CACATTCAAG TAATGTTTGT ACGTTTTGTA
6701 GAGATGGGGT TTCACTATGT TGACCCAGGCT GGTCTCGAAC TCCTGGACTC
6751 GTGATCCACC AGCCTCAGCC TTCCAAAATG CTGGGATTAT AGGCGTGAGC
6801 TACCTCACTC CCTCAGGAGT TGTTTCTC CCTCCCATCC TTAGTCTTCC
6851 CTGAGTAGAC CTGTCACTTA GTCCCCTGGAC CTTTGTGTTT GAAAGCCACC
6901 CTCCAGGCTA CACTCCTCTC GGGTGAGGAG GAGGGTGATC TGGTTGGACA
6951 GGTTGGGCTG CTGTGGCTTC AGGGCACTTT CTCAAGGCTGG GTTGGCTGCTG
7001 CTATGTCACC TTTCTCAAGG AGTTCTGCTG GGACTGGCTT GGCTGCCGT
7051 CTTGACTTTG CTTTGACTG AGGAGGTGGG AGATGGTGAG GGAGGGGGTG
7101 GGGCTAGATC CAAGCCTGGA ATGGGGTGAC CTAACAGACA CTGGGGCCTG
7151 TGCTTAGACA CTAGGATCCT GGGGTTGCA GTTGTCTAGA CTGAGAGGAG
7201 CTGGGGCAA ATGCAGTGTG ACGTTGTGAG AGGGTCAGGG CTGGGTCTGT
7251 GTCAGCCTTC AGGCAGCCTG AGACCAGTCT CTACCTACTC TGTTCCCCGT
7301 GTACCTAGAA AGGAAGGGAA GGTGAGAAGC AATGAGCAGA ATGGAAAGAG
7351 CCCAGATTAA CATGCACATT TCCCATGGCC TTACTGGCCC TGTGACCTTC
7401 AGACACTTTG ATGACATCTT TGTGCTTCGT TTCTGCATCT GTAAATTGAA
7451 GATGTAACA GAGTCTTTCT TAAAGGTTGT TGTGAAGATT ATAGAGCCTA
7501 GCGCATATAA AGCACTTGGC AGAGCCTCG ATAAAAATAAT AGCTGCTATC
7551 ATATTATCAT TATTATTATT TTATTTATTT ATTATTTTAT TTTTTTTGAA
7601 GACCGAGTAT CTCTCTGTCG CCCAGGCTGG AGTGCAGTGG CACAATCTCG
7651 GCTCACTGCA ACCTCCATCT CCCGGGTTTA AGTGATTCTC CTGCTCAGC
7701 CTCCTAAGTA GCTGGGATTAA CAGGCACCCA CCACCCACACC CGGCTATTAT
7751 TATTATTCCCT AGCTATAAGA ATGCTGTAGA GATGAATACA CTGTCAGTGA
7801 GCTAGGAGGT CATCCTGTGT ATCCATCACT TGTGCACTCA GTCGTTCAAGG
7851 CGCTATTGCA TGAACACCAA CTACATGCCA GGTGCCATGC TAAGATTGG
7901 GGACACAGTG GTGACCAAAA CAGACAGAAA CCAAGGAGCT GGCTTACATT
7951 CCAAGGGAGT GCATAGGAAG CTGTGTTCA TTTCAGTTTC TGCTCTAGTA
8001 CCCCCCTTTC CTTGGCAGTG CCAGGGCTG AGAAGGAAGA GTGAGGTGGT
8051 GAGGAGGTGT GAAGCAGTGG GGTGACCTGA GAGGAGAGGA TGGGGTGGCT
8101 TTGCCCTCAAG GCTTGGGCCCT CGTCTAGGTG TCGCTCTGCC TCAGGCCCTCT
8151 GTTCTCCTC CTGACACAGG CACAGACTCG GCCTCCCAAC CCTTCCCCAA
8201 GGACATGACC TTGGGAAGGA ACATATCTGA AGCCCCGGGA GGGTTTCCGC
8251 TGCTGTGCAT CTGTGCCACA GATCCCGAGA TGCAACCCACA GCTGGGAGCA
8301 CCGGTTCCCTC CGCCTCACCT GCACCTCCCTG GTTCTGTTC CTTCTCCTC
8351 CTCCCTCCCT CTCCCGCTC CCCAGACAGG CTGGTGATGA GCTTTATAAC
8401 ATGAAAGCTG ATATTTGGCC ATTATCCTTC TACCCCTGATT GCCAGCTTT
8451 CTCAGAGTGC CTTCTCTGTG AATCCAATCT TTGCAACCGAT TTCCCTGTGA
8501 AACTGCCAGT TTTCTGTATA GGCCTCTGCC CTCTCCTTGG CTCTCTCTC
8551 TGGTCAGTGA GCTTTGTCAA GGGGAACACA GGGCTTCCCTG GACACGTAAT
8601 TCCTCCCACT GAGGAGGAAG GGGCTAATCA CCAGCCCTGT TTTATTTTAT
8651 TTTATTTTTT TGAGATGAAG TCTAGCTCTG TCGCCCCAGGC TGGAGTGC
8701 ATGGCTCGAT CTCGGCTCAC TGCAACTTCT GTCTCCCGGG TTCAAGCGAT
8751 TCTTCTGCCT CAGCCTCCTG AGTAGCTGG GATTACAAGC ATGCACCAACC
8801 ACACCTGGCT ATATTTTGT GTTTTAGTA GAGATGGGGT TTCACCATGT
8851 TGGCAGGCT GGTCTCGAAC TTCTGACCTC AGCTGATCCA CCCACCTCGG
8901 CCTCCCAAAG TGCTGGGATT ACAGGAGTGA GCCACCATGG CTGGCCGACC
8951 CCATCTCTTA AAAAAACAAA AAGAAAAGAA AAGAAAACAA AACAAAAACA

FIGURE 3C



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9001 CTTTTTAAAT TAACTGATT TGTTGGCATG TGCCCTGTAGT CCTAACTACT
9051 CAGGAGGCTG AAGTGGAAAGG ATTGCTTGAG CCCAAGTAGT TGGAGGCCAC
9101 AGTGAGCTGT GATCACACCA CTGTAATCCA GCCTGGGTGA CAGAGTGAGA
9151 CCCTGTCTCA GAAAAAAA AAAATTACTG AGAACTCTGT GACCATGGCA
9201 CCATGAACTA TAGAAAGGGC TAACAGTTGG CTTTGAATG TGGGTTATGG
9251 CTGGGTGCGG TGGCTCACGC CTGTAATCCC AGCACTTTGG GAGGCCAAGG
9301 TGGGCAGATC ACAAGGTCAG GAGTTGAGA CCAGCCCCGC CAACATAGT
9351 AAACCTCATC TCTACTAAAA ATACAAAAAA TTAGCCGGGT GTTGTGGCAG
9401 GTGCCCTGTAA TCCTAGCTAC TCGGGAGGCT GAGGCAGGAG AATTGCTTGA
9451 ACCCAGGAGG TGGAGGTTGC CACAAGCTGA GATCGCACCA CTGCACTCCA
9501 GCCTGGCGA CAGAGCAAGA CTCCATCTCA AAAACAAAAA TAAAAACAAA
9551 AAAAAGTGGT TTGTTTCTT TTCTTTCTT TTTCTTTTTT TTTTTTTTTT
9601 TTTTGAAACA GAGTCTTGCT CTGTCACCAAG GCTGGATTGC AGTGGAGGAT
9651 CTCAGCACAC TGCCACCTCT GCCTCCAGG TTCAAGTGAT TTCCCTGCCT
9701 CAGCCTCCAG AGTAGCTGGG ACTACAGGCA CGCACCAACCA CGCTGGCTA
9751 AGTTTTGTGTA TTTTAGTACA GAAGGGTTT CACCATGTTG GCCAGGATGG
9801 TCTCCATCTC CCTGACCTCG TGATCCGCC ACCTCGGCC CCCAAAGTGC
9851 TGGGATTACG GGCATGAGCC ACCACGCCGC GCCTAAAAGT GGGTTATTT
9901 CTAATTGCTC TCCCCTGATT AAAATTCT CTTTGCCTAT CTTTCTCTA
9951 GATATGTA GACTTCATTC ATCCATTAT TCGTCTCACT TGCTCATCTA
10001 TTTTGCTTT CATTACTCT ACTTTGTTGA ATAATATTAA GTGATCTACC
10051 TGCTGCCAGG CAGTGAGAGT CTGAAGTGA CAGGATGCTG CTTTGCCCTC
10101 TGGGAGCTTA CAGTGTAGCT GGGAAACAGA CATCCAAACAA AGCAGAAAT
10151 TATGAAAAG AAATGTCAGG ATGCTTTGGA ATCACAGAGG AGTGAGAAAT
10201 CCCTCCCGGG GAGGCTGGTG AAGGCTTTGA AGAGGAAGTG ACATTGAGT
10251 GGAGTCTTGA AGACTAGGCA GGATTCTCCA GGGGCCCTGG GTGTGGGGGA
10301 AGCACACATC CTCTTCCCTG TAGGAGGTGC TGTGGAGAAC ACCTCCAGTG
10351 GGGCTGCTAC TCTTCAGCCT TGCTGGGCC AGCTGGAGTG GCCACACCAT
10401 GGTACACACCA GCTGAAGTTC AAGAACCCCC TTGCCAGGAG ATTGCTTTGC
10451 TGGCTCTGGG TGAGGGCAGG TGCACTCTGA AGCCCCCTTC TTTCTAAAGAT
10501 GTTTGCTCCT GAGTTCTAT GTCCTACTCT TTTCTTCCCT GAACCTTTG
10551 CTACCAGTCA GCACAGCCCT GCCTGAGAAAG GAGGCTGGAG GAGTGAGTGG
10601 TCAGTAGCCT GGTGGGTCTT GGCTGCCCT CTGGTGCCCG CTGGCCTAAG
10651 TAGCAGGCTT AGGGAGGCGA GACCCAGTTC CAGGGCTGC CAATGGGGAG
10701 CGAGATGGGG TGGCTGGAGC ACACTGCACA TGTCAACCAAG GCTCTAGGGA
10751 GGTCTGTGCA CAAGGCAGTG GGAAAAGCAA GGGGAAGACC CAGCCTGGTC
10801 AACATGGTGA AACCCCGTCT CTAATAAAA TACAAAAATT AGCTGGGTGT
10851 GGTAGAGCAC GCCTGTAGTC CCAGCTAACT TGGGAGCCTG AGGCAGGAGA
10901 ATCACTTTAA CACAGGAGGT GGAGGTGCA GTGAGCCGAG ATCGTACAC
10951 TGTACTCCAG CCTGGGTGAC AGAGTGAGAC CCTGTCTCAA AAAAACAAA
11001 AAAAACAAA AAAAGTGGG GAAGGGAAAC ACTGATCCTG ATTATCTACT
11051 CCATATACTT ACTATGTACC TACTACCTAC ACAGGGACGG TGGGCTTTAC
11101 GCATGCCATT TATTCACTGT ATAGAGATCT CAGCATCACA TAGGAGCAGG
11151 GAGTCTGAA GTTGGCCTTG CTGGCATTTG AGAAGTTCT TGGTGTATTTC
11201 TTCAAGTCA CGCCTCCAGA CAAGTCAAG TGCTTATTGAA TGCTGACTAT
11251 GTTCCAGGAA CAAACACAGA TGCTAGAAGA CACGCAGTAA ACAGTACAGA
11301 TGCAAGTGCA CATGTGAGGG TCCACACAAG ACCTGAGAGA AGGGAGGGGT
11351 CTTGCTGCAG TTCCCCCTTT GTAACAAAG AGAGAGTACT GTTGACCCCTC
11401 TTCTCTAGGAA CTGTGAGTTT GACTGAAATG TGCTCTGCCA CAGGATCTT
11451 GCTGCTTCCT CTACCTGATT CTTTGGATCT CCGTCTGGC ACCTTCTTGT
11501 CATTCTAGGTC TCAGCTAAAC TGTTACCTCC TTTAAAATGT CTTCTCTGGC
11551 CAGCCAGTCT AAGGTTGCTT GTGCTTGGGG TCTCCTCACT CTCTACTTTA
11601 TCCCCCAGTT GCTTCTTATC ACATATGGCT CTCTGAAATT AGGTATTCT
11651 TACTTACATC TGTCTTCCCC ACTAGAATTA AGCTCTGATG ACAAGGATCT
11701 TTCTGTGCTG TTCATAGCTT ATCTTCTAGT ACCTGGCTTA GTTCTCTGGCA
11751 CATTGTAAGC ATTCAATAAC AGTTTGAATG AATGAATTAA CAAATGAAGG
11801 AATGAATGAA TGCATTTCC TAGAGGACTT CTGTTCTTCC CTGAGGGAG
11851 TTATAGGTG TATTGGTTTC TTGGGACTGT TTTTGTGTTG TTTGTTTGT
11901 TTTGTTTTT GAGACAGAGT CTCACTGTAT CCCCCAGGCT GGAGTGCAGT
11951 GGCACAATCT TGGCTCACTG CAACTCCGC CTCCCAAGGTT CAAGCGATTC

FIGURE 3D



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12001 TCATGCCTCA GCCTCCGAG TAGCTGGGA TTCCAGGAGC CTGCCACAC
12051 GACCAGCTAA TTTTGTTATT TTTAGTAGAG ACAAGGTTTC ACCATGTTGG
12101 CCAGGCTGGT CTTGAACCTCC TGACCTCAGG TGACCTGCCT GCCTCTGCCT
12151 CCCAAAGTGC TGGGATTACA GGCGATGAGCC ACCACGCCCG GCCTGTTTT
12201 TTTTTTTTTT TAAGACAGAG TCTTGACTG TCTCCCAGAC TGGAGTGCAG
12251 TGGGTGATC TCAGCTCATT GCAGCCTCAA CCTCCTGGCC TCAGGTCCAG
12301 GTGATCCTCT TACCTCAGTC TTCTGAGTAA CTGGGCCAC TGTTATATAC
12351 CACCAACACCT GGCTAATTTC TAAATTTTT GCAGAGACAT GGTCTCACTA
12401 TGTTGCCCTG ACTGATCTTG AACTCCCTGG GTTCAAGTGA TCCTCACACC
12451 TTGGCTTCCC AAAGTGTGG GTTACAGGT GTGAGGCCACC ATGCCTGGC
12501 TTGAGACTGT TAAGATGATG AGGCTGGAGG GAGTGGATGG CCTCACTGCT
12551 TGAGCCCTAG AGATTCCCTTA CTCCAGAGTG CCCTGGCTGC AGAGGTGCC
12601 CTGGAGGGTC ACTCCAGCAA CCTGGCTGAG CTGATGGGCA TCATCTGATA
12651 CCAGCTCTGA CCCTGAATAA TAGGCAACAT GGACCTTAGT CTAAAGCACT
12701 GACCCCTCAT CTCTGCATAT ACCAAAGAAC ATGAGATTTG GGTGAGGACA
12751 CAGCCAAACC ATATCAGCTC CGGGGATCCC TGTTGAATG GGGCTTTTT
12801 TGTTGTTGA GGGCTGCACA GGGTGCACCT TTAGGAGGTG ACCTCCGCC
12851 ACAACCCACA GGAGGTGCAC ATGGCCACA CATGCTGGTT TCCTGCAGTG
12901 GGAGGGCTG GGGCACTCCCT GGGACCTGTG CTTGGTAACG GGAGCTGCC
12951 TGGCCCTGGG GATTGGGTGT CTGCCTTGGG TTTCAGGTGT ATTAGGTGT
13001 TCCTCGTTGT GGAGTCTCAT TACTAATGAA AAGTTCAAGGT CGCACTGCTG
13051 GTCCCTTGGG CTGTGGTTGA TCCTGGTGAT AACATTTGGC ACCCAGAGGC
13101 AGCCCTGTTT CCACTGAAGC ATGCGGAGCT TGCGTGGCAG GCAGGCAAGC
13151 TGGCAGCTGC CCTTAACCCA TGAGGTGCTG GCCCGCTAGT AGGCACACCC
13201 TACCTGTGCC AGAATTGAGG TTGTAGCCAG ACTCCAGGAG CCATCTGGC
13251 CCCACAGGGG GCGGCATTTC CTCTTTTGT TGAAACATTG CAGCCAAGTG
13301 CTGGCTTGGG CTTCATCTCT CTGTCCTCACT CTCCCTTCCTC TCCCCAACAT
13351 AAGCCCTCTT CTACATCCTA GAGCTCTTC CATTCCCCCT CCTGCAGCTC
13401 TGGGCTCGCT AATCTCATGC TTCCCTAAGG GAGCTTGACG GCTGCTTCTG
13451 CTAACATTAA ATAAAGTTCT GCGTGCACAGA CCCTGTGTTA TGGGTTTAC
13501 ACCTTATCTC ACAATCTAA AAAAATTCTGAGAAT CCTCTGTAC
13551 CCCCACTTTA CAGGTGAGGA AACTGAGGCA AAGATAGGCT AACTGGCTTC
13601 CCCAACACCA TGCAGGTAAT TAGTGATAAA GGCAAGGTTG GAACCAAAC
13651 TGACCTCCC ATTGTGCTCT TAATGCCAG GACACTCTGT GTCTTGAGCC
13701 ACACTTCCTC CATGTTTCT AGGGCTTCT AGGGAGGCAG ACAGTGATGG
13751 GAAGGGTGT TCTTAGTGT GGATGTGCC TGCGTGCCTC TTTCTGTAAG
13801 CGTCACAGCA CCTCCACTGC TGTACTGGG AGGCACCAAG TTTTCCCTG
13851 TTTGCCACC CAAGGCAGC TAGCTTAGGA GTCACGTGAG TGCTGGTGT
13901 CTCGCCTGCT GCATCCCTCT ATCCGCCCGG TGCCCCCGGT GCCCAGAGGA
13951 GGGCCCTGCC TGTCTCCCA GTTCTCCAAC AGCAGCGCTG TCCCAGCACC
14001 CTCGGCTCC AGTTGTGCC TGGCAGCTGC TGCGCAGAC ACCATACAGA
14051 CAGAGTCACA GCAGGAAGAG GATGGGCCCG AGGGCTGCTG CCTCAGGCCA
14101 TGGCTGCATG GCACCATCAG TTGATTGAGG AGCTTTCTT GCCAATGTCT
14151 GAGGCATCAG GTGGCAGGAC ACCTCCCTCT GCTCTTAAGC CTCAGGCATG
14201 CAGCCCTCTT TATGCTCTCT GGGGTGAGGG GGAGATCCCC CTCATGGAAT
14251 TGCTTTTTTT TTTTTTTTT TTGTTTGAG ACAGGGCTCT GCTCTGTCAC
14301 TCAGGCTGGA GTGCAGCCTC AACCTCCCAG ACTCAAGTGA TCCTCCGCC
14351 TCAGGCTCCC GAGTAGCTGG GACCACAGGT GGACACCATC ACACCTGGGT
14401 TTTTTTGTGT TTTGTTTTTT GTTTCTAGA GATGGGGTCT CACTTCTTG
14451 CTCAGTCTGG TCTCGAACCTC CTGGCGCAA GCAGTCCCTC CACCTCGCT
14501 TCCCCAAAGTG TTTGGATTAC AGGTGTGAGC CACTGTGCTT GGCCTTTTA
14551 TTTATTTAGA ATTTGTTTG GAATTGCTTC TTTATGCCCTG GCACTATGCT
14601 GGCACATATGT GGCAGAGATT TTAAAAACGA GCAAACAAA CAAATGCTT
14651 GTCAACCACA AAATGTATT TCTGCCCTT AGGTTCTTT TGTGTAGTTG
14701 AGGCTAGAAG AAAAAATAG GGGCGATGAA GGAGCAGGGGA GCGATGGTTT
14751 AGGAGGTCTT CCTTCCAGCC CCTTGTGTTA AGCATCTGGC TCACTAGCTT
14801 GGGGAGCCA TTAGGCAGCA GTGGCCAATC CTGAGGCACT CTCAGGTGTC
14851 ACTAAGAAAA GGGGCATGTG CTCTATGGAT ACCCATGGC TGAACCTGGA
14901 GTCTGGTCTG GACCCATGGC TGTGCTAGGA TCCACCGTCC CCAGCCCCAA
14951 CTGCAGTCAG CATGTTCATC ATCCTTAGGC CTCTCCGCTT CTTCTGCAT

FIGURE 3E



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15001 GTTTGTCTGC CTCATGCCCT GCTCATTACC AACTGGTCAG TCCCCACTGC
15051 CCTGCGCTGGA GTGAGCTGGT TTGATTGGCT TAGCTAAGCT CCCTTGCCCTC
15101 TGCTGGCCAG GTCACCCCTGT GGGTCACCAAG CAAACCTGTT GATGGTCCAG
15151 TCTGAACCTG CTTCTCCACA AAGAACATGT TGCACCCAGC CCTGCTTCTC
15201 TGAGCAGAGG TTTGGGGCTG AGCTGTTCTA GCCAGAAAGG GACACAGGGT
15251 GTGGCAGGCA CCATGATGGG CATATCTAAT GTGCCGGGAA AAACAATGAG
15301 CTGCTCTCCG TGCTTTGGGC ACCTGGTTGG GAGAGGGCCC ATCTGTCTGA
15351 CTTTCTCCTC CTGGGGCTCT CAGCGTCTCC GAGAACCTCT GCCAGAGCTG
15401 TGTAGAAGTG GTTGTGTTGT TTCTTAACAC TTCTGTGCCCT TATTCTTTC
15451 TGTACCCAAG AAAGGAAGTA GACTGTTTTG TAGGGACACT GTCGGGGTGA
15501 TGAATCTGGA CTTACTGGAA TCATGAACCA TGCCAAGGAG GAAGGAGAAA
15551 ATAGGCTATG GTGGGTGTCT TAGTTAGGGC TGGCTGCTGT AACAAAATGC
15601 CTTTAGCTGA GTAATTTAAA GCAAGAGAAA TGTATTGCTC AGAGTTGGG
15651 AGGCTGGGAA GTCCAAGATC AGGGTCCAG CAGATTCACT GTCTGGTGA
15701 GGCTGATGCT CTGTGACAAA GGTGGCACCT TCTAGCTCCA TCCTCACATG
15751 GCAGAAGAGG GAACAAGCTC CCTCAGACCT CTTTCTAAG GGCAGTTAGTC
15801 CCATGCATGA GGGCTCTAAC ATCACGACTG AGTCACCTCC CAAAGCCCTC
15851 ACCTCCCACC AGCACTGCAC TGGGGATTAA GTTCAATAT GGGAAATTG
15901 GAGGAACACCA GACCTTCAGA CCACAGCAGC GGGCTTCTCC TCATGTGCC
15951 CCTGCTCAC TTCTAGATGC CGCATAATGT CAGTGAAACC CCGTCTCTAC
16001 TAAAAATACA AAAAATTAGC TGGGTGTTG GGCACGTGCC TGTAATCCCA
16051 GCTACTTGGG AGGCTGAGGC AGGAGAATCG CTTGAACCCA GGAGGCAGAG
16101 GTTGAGTGA CTCAGATCG TGCCACTGCA CTCCAGCCTG GGCGACAGAG
16151 GAAGACTCCG TCAAGAAAAA AGAGAAAAGG CATCAGGTAT GCCAGGGTGT
16201 GCGGAAAAG GCATCGGGTA TGCCAGGGCG TGTGGAAAAA GGCATCGGGT
16251 ATGCCAGGGT GTGTGGAAA AGGCATCGGG TATGCCAGGG CATGTGGAA
16301 AAGGTGGTAA GATTCCCTAG CCTCCCAGGG TTGGGAAGCC TCTGGCGAG
16351 TGAAGCATAAC CTTGGGTGGG TTTTAAGACA CCAGCTTCC AGTCCAGCTC
16401 AGCTGTGGGA TGTGGGAAACA TGAGTCAGTG GGAACATGAG ATTGGCTTC
16451 CCTGTGGCTC ACAATAATAC CTACTCCCTGC CTACTTCATG GGACCCGCAT
16501 AAGAGCTGAG GGATTCCATA GCTCAGGGGT ATGCTGTAAA GACAAGCACT
16551 ATGCACCTGG GTGTGGTTCT GAAACTTCT TGTGCAGAAG AGTGAGTAGG
16601 GCTGGCGAG TCCTGAGAAT GTGCATTCT CACACACCTC TGATGCTGCT
16651 GATGCTCTAG TCCCTTGGCT GGCAAGGGTA CCTGGTTAGT AGGGGCCAGG
16701 ACTCTGTAAT GCCTTCCACT TCAGGGTTCT CTGGGCTGGT TTTCTGACT
16751 CCCCAGGAAG CTTTATTCA GCAGAGGGAA GGTAGGAGTG AGAGGACTAC
16801 GCTGTCAGTG CTTCACATAAC ATCGTTAAT TTATCCCAGC ACAGCCCTTA
16851 GGAGGAAAGC AGTATTCTCC TTCTACACTT AAGAAAATCG GCCTGGTGC
16901 GAGGCTCATG CCTATAATCC CAGCACTGTG GGAAGCTGAG GCGGGAGGAT
16951 CGCTGGAGCC CAGGAGTTCA AGACTAGTCT AGGCAATACA GGGAGACCTC
17001 ATCTCTACAA AAAAAAAAAA AATTAGCTGG GCATGGTGGT GCACACTTGC
17051 AGTCCCAGCT ACCTACCCAG AGGCTGAGCT GGGAGGATTG CTTGAGTCT
17101 GGAGGATCGA GGCTGCAGTG AGCTATGATT GCTCCACTAC ACTCCATCCC
17151 TGGCAACAGA GTGAGACTCC ATCCCCAAAAA AAAAAAAAAA TTGAAGCTAG
17201 GAGAAGTTGA GACTTGCCTG AAGTTACACA GTAAGTGCNA GAACCAGGAC
17251 TTGGACCAAG TCTTCTGAC TCCAGGCCAA TGATGTTTC TTCCATGACA
17301 TATATAGCTC TTGAAACTAC TTCTATCTAA TATCACCCAC AGTGTGTTA
17351 AAAATACAGA TTTCTGGGC TCACCCCTCAA ATTATGATTG AGTAGGTCTA
17401 GGCACGTCAA GGTCAATTGTT TTTGTCTTGC TTTTAAGTC CCCCAGGTGA
17451 TTCTAAAGCC GAAGCTCTGC AAAGCACACC TTGAGAAACA GAGAACTCTT
17501 GTGCTCTCGC TCTCTTGAC CTTCAAGGTGC AAAACTTTG TCCTAATGTC
17551 GTTCTCAAAC TTACGCTATGT GTGAGAATCA CTGTGAGAGC TTATTGAAAC
17601 TGATTGCGGG ACCCCATACC TAGAGGGCCT GATTCTATAG GTCTGAGGT
17651 AGGCCAAGA ATTTGCAATAT TTGCAATTGCT TTTTCTTTTC CTTTCTTTTC
17701 TTTTTTTTTT TTTTGAGAT GAAGTCTCAC CCTGTCGCC AGACTGGAGT
17751 GCAGTGGCAT GATCTCAGCT CACTGCAGCC TCTGCCTCCT GGGTTAAAGC
17801 GATTCTCCCC ACACCCCAAGA CCCGCTCCTG AGTAGCTGGG ATTACAGGT
17851 CCCGCCACCA TGACTAGCTA ACGTITGTAT TTTTAGTAGA GACGGGGTT
17901 TCACCATGTT GGCCAGGCTG GTCTCAAAC CCTGACCTCA GGTGATCCAC
17951 TCACCTCAGC CTCCCAAGGT CTTGGGATTA CTGGTGTGAG CCACCGCGTG

FIGURE 3F

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18001 CGGCCAGAAT TTGCATTTCT AACAAAGTCCC AGGTGATGCT GATGCTGTGG
18051 GTCCAGGGAC ACACTTTGAG AACAGCTTGT TACTCAGGCG ATATGTGGAC
18101 AGTAGCGTCA TCTTCACCTG GGAGCTTCCT GCAGCATCTC AGGCCTTGCC
18151 CTACACCTAC CAGATCAGAA TCTGCATTT AACTCAATCC CCGCGTGATT
18201 CTCATGCACC TGGAAAGTTTG AGAAATATGA CCTTAGAGGA GCCGGAATGT
18251 GAAACCACGT GAGGCAGAGA TAGATGGAGA ATATCTCTTC TTCTCACCGA
18301 TACTAAAGAT GCAACAAAAA GGGCTGACTC TCTGGGTGTG CACCCAGGTG
18351 GGGCTGATGA CGAAAAGAG GCCAGATGTG GACAGAGGAC TCTTCCCTGA
18401 GGGAAAGGCAG AGAGAACTTA GGAAAATCTG AAGAAAGGAG GTGGCTTCAG
18451 AGGAAAGGCA TTCATCTGGG CCATAAAACA GTGGAGAAGG TATCCTGCTG
18501 AGAGCACAGG GGTGGGGAGG GGGTGCCCTG GAGCTGAAGT CTTCACTGGG
18551 GGGACAGTGA TAGGTGAACA CACATGTGAA TAAACAGTTT GCTAACAGCAGC
18601 TGCGAGGGCT GCCCAAGGTG AGAAAGCATC CGTCTGCAGA GGCCTCAATA
18651 AGGCCAGTGT GTTGAACCTTG TCCTGCAGTG CTCAGCAGTG GAAAAAAACCA
18701 ACAGCCACGC AGGGAGAGGG AAGGAGCCAC GATGGGCACG GGTTACTGGG
18751 GCCAGGGCTT GACTGGTAGG TGGACACAGC TGAAGGGCCA GTTGTGTGG
18801 GAACAGAGCG CAGAAGCAAT AGATTCCTCT TGAAGATCCT TGGGCTGTTA
18851 ACCTTTTTA ATTAAAGAG AGGTTGTGTG GGCGGGGGAGG GAGGAAGGAA
18901 AATCCTTCAG AAGACATAGA CTTACTCTGT TTCTTCCATC ATATGTGAAT
18951 GCATATGAAT AGCCAAAAGG TGAATAAAAC ACATGTTCCC AGGTGGCCAG
19001 TGAGACCTAG GTTGAACAGT GGTGGGTGTG GTGTGAGGCC GGGGAGTGT
19051 GCGAGCCCCG GAATTCTCA GCCTTAGTCC CCCGCCACAT AGCTAAAGAAG
19101 TGAGGGAGGA GGTGAGAAGG AGTCACTGCG CAGCCTCACT TCCGGTGGAG
19151 TACCTCTGTCT CTTGTCAAGT TCTGTCTCTG GGGACAGTTG CCTGCTTCA
19201 CCTCTCCCTC CATCCCTCT TCTCTCACAG GGAAAATTC ACCTTAATAT
19251 TCCAAGTTC TCTCTAGCA AAGTCCCTCT CAGGCACCCA CAGGAAAAAA
19301 GGAAACTAAG CAGAGTTAGG GCTTCAGGC CTAGCCAAC ACTCGACTCT
19351 CCTCTTGCTT CCCTAAGAAC CAGCGCAAGG GGCAGCGTGG GTTCCAGCAT
19401 AGATGGACCT GTGTTGAAAT CTC TGACAGT GCTGTGCTGA CCTGGCTAG
19451 CCATTGACCT CTCTGAGCCC TTGTTTCTT TCCACTAGGC TCTCTGAGGG
19501 CAGGGGCCAT GTCTTTTCA CTGCTCTGTC TGCACTGAGC ACTGTGCAGG
19551 GCACATAGGA AGTTCCCATA AATGTTGTG GGATAAAAGGA AATAAAACCT
19601 TCTCTCTTCC TGTCCCCCTT GTGATGGCTT TGCAACAAGGC ACTGTCTTG
19651 GCCAGGTTTG CTAGGCTAGT GTGAGGATAA ACCAGGTATA TTACAAATTG
19701 GAGAAAATTTC TCGTTCTTC TTGGAAGAAG GTGCTGTATC ATGAAACAAG
19751 AATGTCTTGA TTCCCTTCTA TGCCAGGTAC TGGGGAGAAA CAGGTGCCTG
19801 ATAACCCTTG ATCCAGGCAG AAATAAGCAT ACTCCTGCTT CCCAAGGCC
19851 GATGCTTCTC TCCCTCCTCC CTTCCCTCC CTTCTCTTC ACTCTTCTC
19901 TGCACACATG GAAGAATGGC TGCCAGGCAT TGCCCATTTG GAAAAGTACA
19951 GCTCAATGGA TATGAATCACT CTTGGCAGG CGAGAAATGA TTCACGTCTG
20001 ACCAAATCGA TTAGTTCACT GTGCCCGTT CTGCATCTT TTTCCCTTGT
20051 AATTAATGA TGATTGGTCT TGATGGTGGG AAGGAAGAGA CAGAATTAA
20101 TTTGTTGCC TTTGTAGAAA GCTGGGACA GCACAGATAA GGGAAAGATGT
20151 CTCCCATTTG GCAAATAACT GATGCCGGAGG TGGAGTGGCA GTGGTGTAG
20201 GGATGCTGGT GCCTTCAGGC CTCTGGGCC GGGCAGTGCA GCTGGTGGCA
20251 GACGGTTCGG AACTCTACCA TGTTCCCATC TGAATAACTGTG GGCTGATCAT
20301 GCCCACTCCT GACCTTGCTC CAGGGAGTAC ACAAAAGACGT AAGCTTAATT
20351 AACCCACCAG ACGTAGCTCT TGAATCCCTG GGCACTAGTGC CTGGGTATAG
20401 TTAGAGTTGG GGAGAGGCAT GGTCAAGAAA ACAACCTCCC TCATCTCT
20451 GTTGTCACTC AGAGTCAAGC TGGCTGCTGC TGTTGGTGCT GACTTCTCTT
20501 GCTGCAGATT TCTCCAATAT GTTCTGCCCC TGACAGCATT TGCCAAATCC
20551 CTTCGGTTTC TTGTGTCTCG TGCACTGTTA GCTCCTCCAG CCCTTGGATG
20601 AAGAACGCTG GGAACCTTT GCTTCCTTCC CCTCCCGCAG TGACATGCCA
20651 TGCCATGCCA CTGCCCTTCA ATCTGGTCTT ATGACAGTCA CTCATAAGCA
20701 CCCGCATGTA CCCGGCCCTG CACTAGCTCA TGACAGCTGC AGTCAATTGG
20751 GCCAGGTGCT GTATCTCATC CGGCCTCCTC AGCAACCCCTC TGAGATACTG
20801 GTAATGTCCC TGATGAAGAT ATTTACTGAG GCAGAAATGG ACGCTCAGTG
20851 AAGCAAGGTG CCTGATGTTA TAGCAATGAG CTATGAGTGG CCAGAGGGAG
20901 GAGATAAGCT CAGGCCCTGAC ACCAAAGCCC ATGCTCCTTC TAGTCAACCA
20951 CAGTGCCTCC TATGGTGAAT GAGTGAAGTCA GCAACCAAGA CGCATGAGGC

FIGURE 3G



Docket No.: CL001188

Serial No.: 09/817,198

Inventors: YE, Jane et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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21001 CTTCTTTTG GTGAGCCTTG GCTGGGTGCT GAGGCTTCAG GTACAATCAT
21051 GGGTTGGAAG AGCCCTCCTC TCTCTCCACA GTCTGGCACT ATGACCCCTT
21101 CTGGTTATTA ACAAGGCAAA GAGAGAGAGG GAAGAAAGCA GGCAAATAAT
21151 GTGGGTTGCT ATTCTTAGAG ATTAGAATT CAGGAAGGAT AAACACAGCG
21201 TTCTCTCCAG AAGTATAAAAT AGGAAGACTT CACACATGAC TAGAACGAGA
21251 CATGTTTAA GTCTGTCGAG TAAGGCAGTG ATGAAGTAGA TTTCCCCAGA
21301 TTCACTCTCC CTCCCTCTGGG TCCCCCAGGG CCTTACTTG TGGCAACTT
21351 CAGCTCAGGG AGGGAGGAAA GCCCCTTCAGA AAGCTTCAGA TACTTCCTTA
21401 AGGTCAGTTT CTGCTTAAAG AAGGCCCTTA CATTACTTCA TCCCTTGC
21451 AAATTAACACT GAAAGGAAAC CTTTCAAGTG TGATTGCCTG GCCCTTCC
21501 GTTCATTCT CGTGGGTACG CTTTCTAATC TTCTTCTTCTT CTTCCCTTCT
21551 TCAGGTGTTG ACTTTAAGAT GAAGACCATA GAGGTAGACG GCATCAAAGT
21601 GCGGATACAG ATCTGGTGAG CTGGGGAGGA GGAGGAGGCA GATGTAGGAG
21651 AAGAGGACTT CTGGCTGCTC CTTAGCTGCC CTCGCCATGT GTAAAATCC
21701 TAGGCTTCAC CTGGGATAAC TGCCACCTC TCTGATGGAT GGAAGCGAAG
21751 TCTCAGAAGC CCATCTCTTC CTATAAGCCT TAATCTCCAA CCTCTAAGAA
21801 ACTTTAGGGG ATTGACTACA AGCACCAAAG GGAGGAATT AGAAGGAAC
21851 GGCACACTAA CCATTGTGAA TTTATCTCAG GATTAGGCTT TGCCCTTGGG
21901 CTGTCACCA CTATGTTAAG ATTGGAAGGA AGGAGGCTAC ACCCCCCATC
21951 ATTTAGGGCG AGACCCCTGAG AGAGTTCTC AGGATAGCAT GATGAAGTTT
22001 CCACAGTAGC AGAGGGTGCT GCTGTGGCTC TCTGCCAG GTCCTGGAAAG
22051 CACTGCCTT GCCAGGGTTT AGAGCTCCCT CTCATTCCA CAGCAGTATG
22101 GGCACGTGCCT TCAGAGGTCC CATAGGGACT AGGGGTGTAG CAGCATCCCC
22151 TGCCAACACTCC CATCCAACCA AATCTGGCCA CAGTGGCCAG ATTCCAGAGA
22201 GCTGTCCAAG GCCTGTTCTG GCTGTGGCTT CTGGTTCTG CCAGGAGGGC
22251 AGTTGGCAGG AGGGGCAAG GCCCCTGCAGG CCTGGTCAGC ACCAGCACAG
22301 ATGACCAAGGC CTCTGACTGC AGATCCCTGT GGGGATCCAA GCATCCCTGG
22351 TTTTCACCC TTAGCTCCC CAGTTTTCTC TACAAGGGGA CAGCTCTGCT
22401 CTTCCCCCTCC CCGTCTGTTCC CCGATGGCTCC TGCTCCTCTG AGGGACTGGC
22451 TTTCTCCTGC AGGGACACTG CAGGGCAGGA GAGATACCAAG ACCATCACAA
22501 AGCAGTACTA TCGGGGGGCC CAGGTAAGCC ACCACATTGG GGGTTCAAA
22551 GTGGGAAGCT GCCACCCACA CTCCCAGCTC TGTTGATTTG AGATGTCGT
22601 GCCACGGATC CCCTAAATAC AGTTCCCTG CTGGGAGGAG CGCAGGGCGT
22651 CTTCAGCTG TTCACTGATC ATTGTCCGT CCATTGTTCA TGGCCCACTC
22701 ACTGCAGGCA GGCCCCCTGCC CTCACCCCTG ACTTCCACCC TCCATCTGG
22751 GTCAAAGATC CAGGTCAAAG CATGTGGTGT CTTCCTGCTG TAGAGAGTTC
22801 TGTGATGGGC CTGGGAGGGC GCAGTGGTGG GGTCTGAGAG AAGAGATATT
22851 TCTGGATGCT GAGCAGGGAG AATGGGAGAG TGGGACCCAA CCTTTAAGTT
22901 TCCACGGCCC CTTCTGGCCC CATGACTGCA CTCTCTCTGT GCATATCAC
22951 TCTCTCTATT TCTCTCTCTC TCAGGGATA TTTTTGGTCT ATGACATTAG
23001 CAGCGAGCGC TCTTACCAAGC ACATCATGAA GTGGGTCAGT GACGTGGATG
23051 AGGTAGGAGA TGCCACCTCA CTGGGGGGT GTGGAGAGGG TGCCTCACCG
23101 GGGAGGCAA GGCGAGGGGCC AGATGGAAG GCAAATGCTT CCAGGAAGCT
23151 TTGCTTCCA CAGCCCTGGA TGAAGACCTC TGTTGAGTA AGACATGGGG
23201 AAGAACCGA AGCTGCCATG CCCTCACTCT CTATACCCCTG CCAGGCCCTC
23251 ACGGCTGTGT CTTCCCGGA AATGAATTAG TTCAAGTCT TCCCTGTGAG
23301 CAGCTCTTCTT CCTGAAATCT TGGGACCCAGG TGGAGTTGCA AGATTGGGAT
23351 CTAGTCTCTGG CTCTGCACAA TAGCTGTGGA GCCCTGGGAA GCCATTGAA
23401 TCCTCTGGGT CCCAGTTCC TGTAGAATGA GGCTGGACT TACATCCAAT
23451 GTCCCTTCCA GCTCTGATAC CAGTGGCTCA ACCCAAGGAA GCACCGACT
23501 TAGCCAGAGT GTCTTCTACC CTAAGCTCTC CCCGTGATAC CCTTGAGGTC
23551 AGCCATGGCA CTTGGGGAGG CCTGGCACCT GCATCCAGTC GGCCCACCC
23601 GTCCCTAGGG CTCTGGAATT GGTGGTGGC TGAGGGCAGT GCAGACTCTG
23651 TAGGAAAAT TGGGGGGCA GGCAGCACTC ACTGGCTGTT CTGCCCATCC
23701 TTTGCTCTA GTACGCACCA GAAGGCGTCC AGAAGATCCT TATTGGGAAT
23751 AAGGCTGATG AGGAGCAGAA ACGGCAGGTG GGAAGAGAGC AAGGGCAGCA
23801 GGTAGTGGA GGGAAAAGGC AAGTCCACCC CAGGTCTCT GCTGGGCC
23851 CAGGGCCAGT CTCAGCGTGT GGGACCTAGG GGTGTGTTCC CCAGTGGCAG
23901 GTCCCTCCAC ACGTCCCCAG CACCCCAAGG CCCTGGGGGA GTGGCCATCC
23951 TCGGAAGGCT TGTTGTCTGG GTTCAAGGAC AGAAGCCCAG AGATTGGGG

FIGURE 3H



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24001 TCCATCCAGA AACAAAGACG TCATAGGCAG CAACTCTCCC AAGTCCAGGT
24051 CCCCAAATGC AGGATTGCC TCTGCTTAAG AGATCATCCC CGTGTAGTA
24101 ATGAAGGACT TCAAGTTGTC AACCTCTTCT CTGACAGCAT CCAGGCCTAG
24151 CTGCCATGTT ACGGTCGAGA AATGATCTCC CATCCCACCC AACACTCCCC
24201 CACTCCTGTC CTTCTTACCC AGGAAAGAGC CAGGGAGGCA AATGAGGAGA
24251 CAAAGAGCCA CAGCTGGAGA AGCCATGGGG GCAGAAAGGG TAGGAGGATG
24301 ACGCTGAGGG AATGTCCAAG CATGCAGGG AACCACCTC CCAGAGAGCA
24351 GAAAGAAATA TTGGTTATTT TTTTTCTT TCTTCTTTT TTTTTTTTT
24401 TTTGAGATGG AGTCTCGCT TGTCACCCAG GCTAGAGTGC AGTGGCGCCA
24451 TCTCGGCTCA CTGCAACCTC TGCCCTCTGA GTTCAAGCAA TTCTCTGCC
24501 TCAGCCTCCC AAGTAGCTGA GATTACAGGT GCATGCCACC ACGCCTGGCT
24551 AATTTTTTG TATTTTAGT AGAGATGGGG TTTGCCATA TTGGCCAGGC
24601 CGGTCTCGAA CTCCCTAACCT CAGGTGATCC ACCTCCTCA GTCTCCAAA
24651 GTGCTGGGAT TACAGGCGTG AGCCACTGTG CCCAGCCAAG ATTGGTATTT
24701 CTGAGATAAG TTATCCACTC AGTCCGTGGA CCTCAAGAGT TTTCTCTCC
24751 CTTTCAGTC ATAGCGTTC CATTAGTACT TAAAATGAAA TTGATTGTTT
24801 GGTATAAAAT ATAAGACATG GTCATTGACC AATTGAAAG TAGAGGCAAA
24851 GCCTACTAGG ATAGTATTTA TTGAGGCACT TATGTGTGGC ACTGTGCTAA
24901 GGCAAGCGCT TTTAAGTGCA CGACCCACT GAATCATCCC ACAACCATGG
24951 ATGGGAGACA CACTCAGTCT CCTTTAACAG AAGATAAAGC TGGGGCTTAC
25001 AGAGAATGTA CAACTGTCC AAGGTACAC AGCTAGCCAT CAGTGGCAGT
25051 GCTGCTATTG AGGTCTGGGA CTGTGGGACT CCAGAGGCCA TGTTTTTAC
25101 GAGGATGCCA TACTGCCACA ATGGATGGTG TCTTATCTC CTGATATATG
25151 ATTGTGTGTT GGGAGGCCTG GGGTGGCAGC TGAAGAATG GAGAGGCATA
25201 TTTGTGGAGG ATCTTCCCCC ATTCTCTGCT ACCCTCTCTT GGAGCTCCCA
25251 GTCCCATCTG AGAAATTATC TACTCTGAGA AATCGTCACA ACACAGCATG
25301 GTTGTGAGTG CAGTGGCAGA AGCCTGTGCC TGTTGTATG GGCCCCTCCC
25351 CTGCCTTACT GACTCTCTT CAGAAATGTC CTTCTCTGC AGCTGGCGAA
25401 GGAGTATGGC ATGGACTTCT ATGAAACAAG TGCCCTGCACC AACCTCAACA
25451 TAAAGAGGT GAGAGCCCTG GTGACCAGGC GCCGCTCTC TCGGGCTGAG
25501 TCCAGCAGAG GTGGGAGGAG GAGCCATAAG ATGGACCTTA TCCCTCAGGC
25551 CGCTGCAGGG TTGCCAGGGG AGAGGAGGAG ACACCTGGACT AACCTGTGCC
25601 CTTGGTTTC CAGTCATTCA CGCGCTGTGAC AGAGCTGGTG CTGCAGGCC
25651 ATAGGAAGGA GCTGGAAGGC CTCCGGATGC GTGCCAGCAA TGAGTTGGCA
25701 CTGGCAGAGC TGGAGGAGGA GGAGGGCAA CCCGAGGGCC CAGCGAACTC
25751 TTCGAAACC TGCTGGTGT GAGTCCGTG TGGGGCACCC CACACGACAC
25801 CCCTCTTCCC TCAGGAGGCC CGTGGCAGA CAGGGGAGCC GGGGCTTGC
25851 CCTGCTGCTG CCTCTCGTG TGATGACCT ATTGAGTATC AGTAGCCACT
25901 ACTCCCCCTG CCTGGCCCTG AGAGGGCTC TGCTGTATC TCAAGCAGCC
25951 CCTGTCCCCA GCCCGTCCAC CCTGGAGTGG TCTTCTTCAG CCTGTTTCCC
26001 CAGCCACAGG CCTGCTACGA CCCCCACGAT GTGCCGCAAG CACTGTCTCA
26051 CCATCCCGCA CCCACCAGAC AACAGCCAGG GCTGGAGTCC AGGCCACTTT
26101 CAGCTGCTCC TTTCTCCGTG CATCGTGTCT CTTCTCTGCT TTTTCTCTCT
26151 TCCCCCACTT CTCTTCTCT GACCCCTCCC CTCCGGTGC TGTCGTATCA
26201 AAGCTCCTCA AACCCCGTCC CCGGTGTGTC TGCTGTGTG CAGCTCGCTC
26251 TTTCTTCCCT TCCTAAGCTA TCCAAGGGGA TGACCCAGG CTCGTGGGGA
26301 GGTTCCACCC TTGGATCCAG GAAGAACCCCT CCACCCCTGCC TCGTGGGTGG
26351 GCCAAAGGCT ACAGGGTGTCT TCTTCTCTT CCCCCACCC CACTGTCCCT
26401 CATGTGCCAT GGGCCTGCCCT CCCCAGTGAC CTGCGAAAGT GGAGCATCGA
26451 GGTAGGAGGG AAACGGCAAC CAGGGAGTCC TCGAGCCTGG GGCTGCCCTA
26501 CCTCTACCCA TTCCCCGCC AGAGCTTGC CTTGCTTGG CTGCCCCCCT
26551 GCCTCTTGG GGAAGTGAGC TCAGAGGAGC TGCTTCAGA GAAGGAAACA
26601 AAATGAGGGG TGGCAGGGGT AAAAGTCAC CTCCATTCTC TACCTCCCAT
26651 GCAGCATGAA CACAATTCT CTCCACCTGG CTCCCAAATT TAAAGATGTG
26701 GACCAAGGCC TGTGGGTACT CCAGGGGCAA GGAGAGCCCT GGGGTCAGTG
26751 ACAGTCAGGCC CCAACCAGT CACTCCACAA AGGGGAGCAT TTGGAAATGA
26801 AGGACTAGCT CCTATGTATC AGGTTAAGAG CAAGGGAGAG CTGGCCAGGG
26851 ACAGCAGTTT GCACAGCAGA GGGGAATGTA GCAACAGCAG GGCCTCCCTAG
26901 GCCCATCTT CAATTCTTA GTTAAAGAAGA GCATTCCTC AGACTCCAG
26951 GCGGAGGACT GAGCCTAGCC TTCAAGCAACC AAGGTTCTCC TGGGACCCAA

FIGURE 3I



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27001 AGTTTATGGG AGAAGGGCAA AGACTTCATG GGAAGAGAGA AGGAAGGCC
27051 TGGGTAGAAA CGCTTGGTGC TGTTCTCTT GGCCCTTAAG ACAAAAGCGCT
27101 CATCTTGCCTC TCTACCTCCCT GATAGGCTTG AGGGTTGCC AACCACACTG
27151 TGGCTACAGG TGGAGGGAAAG AGGACTCCCT CCTCCAGAGT GCTATGTTCA
27201 GGAAGTTCT TTAACCCCCAT ATGGCCCAAG AGTAGCTCGT AGGAGGCCCT
27251 TTAAAGACGG ACAAAGTAAT TTACCAAGTTC TACTGGGGTT CCTGCCACC
27301 GTCCAAGGT GGGCGAGGCC TAGGAAGAGG GTCATTCTTA AGCCACACAT
27351 TAGCTGCACT GCGTGGCTGC AGCCAAAACA AAGAACTGGG TGTTGAGTAT
27401 TCATCAACTA AGAACCAAAA TCCAGGGCAC TCATATGTGA AGGATAAGAA
27451 CCTCACTTCC TTACTCCTCC AAAAAGAAGT GGGGAAAGAA CCATCAAACC
27501 TTTCCCTCCTG ACTTACCAAA CCAGGAAAC AGCAGGAGAG GGTGGCTCAG
27551 GACTTAGGGA CAGGGTATAG CTTAGATGGT GGAAAGCAAA GGAGAGCAGG
27601 AAGTTGTAAA TCACTGGCTA ATGAGAAAAG GAGACAGCTA ACTCTAGGAT
27651 GAAGCTGTGA CTAGGCTGGG GTTGCTTCCT TGAAAGATGGG ACTCCTTGGG
27701 TATCAAGACC TATGCCACAT CACACTGGGG CTAGGGAAAGT AGGTGATGCC
27751 AGCCCTCAAG TCTGTCTTC GCCAGGGACT TGAGAAAGTTA TATTGGGAG
27801 TGGCTCCAAT CTGTGGACCA GTATTTCAGC TTTCCTTGAA GATCAGGCAG
27851 GGTGCCATTCT ATTGTCTTTC TCTCCTAGCC CCTCAGGAA AGAAGGACTA
27901 TATTGTACT GTACCCCTAGG GTTCTGGAA GGGAAAACAT GGAATCAGGA
27951 TTCTATAGAC TGATAGGGCCC TATCCACAAAG GGGCATGACT GGGAAAAGGT
28001 ATGGGAGCAG AAGGAGAATT GGGATTTTAG GGTGCAGCTA CGCTCACCT
28051 AAACCTTTGG TGGCCTGGGG CATGTCTTGAA GGGCCAGACT GTTAACCAGG
28101 CTCTGCTGGC CTGTTTACTC GTCACCAACT CTGCACCTGC TGTCTTGAGA
28151 CTCCATCCAG CCCCAAGGCAC GCCACCTGCT CCTGAGCCTC CACTATCTCC
28201 CTGTGACGGG TGAACTTCGT GTACTGTGTC TCGGGTCCAT ATATGAATTG
28251 TGAGCAGGGT TCATCTATT TAAACACAGA TGTTCACAAA ATAAAGATTA
28301 TTTCAAACCA CCGGTGTGGC TGCTGGAT AGTCCTTGGG GGTAGGTCTC
28351 ACTCAGACCC TGGCAGTGTAGT GTGGGAGGGAGA GAGAGGCAGT GCTGGTAGAA
28401 GCAGCTCCAG AAGCAAAGGC AACAGCAGTA GAGTGACCCAC GGAAGCGGCA
28451 AACATTGTCT TCCCTTCTCT ACCTTCCCTA GTGCCACCTG CAGGGAGGCC
28501 CAAAGCAAAG CCCCGTTGCC CTGCATTGGG CTGGCACTGC AGAAATAAGA
28551 TGAAACACAG TTATCGAGAG GATGCTGAAC ATCTATGAGC AGGTTTAA
28601 GCCAAGATGA GTCTCATCTG TTTGTGTGGG TCAGGAACGG GTCTTCTGA
28651 AGGCATGAGG TGGGACTGGG TAATCTTCA GATTGTGAT TGGATAACCTC
28701 GGGGAGCAG AGGCAGACTG GGATCTCAGG ACTGCAGGTA TTCATACTT
28751 TGGGATATGG AATTGATGGG (SEQ ID NO:3)

FEATURES:

Start:	2044
Exon:	2044-2167
Intron:	2168-21554
Exon:	21555-21615
Intron:	21616-22462
Exon:	22463-22523
Intron:	22524-22974
Exon:	22975-23052
Intron:	23053-23711
Exon:	23712-23801
Intron:	23802-25392
Exon:	25393-25458
Intron:	25459-25613
Exon:	25614-25769
Stop:	25770

CHROMOSOME MAP POSITION:
Chromosome 14

FIGURE 3J



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ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
206	-	T	Beyond ORF(5')
4963	C	T	Intron
8175	G	A	Intron
10515	T	C	Intron
13034	T	C	Intron
13781	T	C	Intron
14050	A	C	Intron
14273	-	T	Intron
17582	T	C	Intron
17700	C	T	Intron
18074	T	C A	Intron
19328	G	T	Intron
19570	A	G	Intron
20892	C	T	Intron
26465	G	A	Beyond ORF(3')
26472	A	G	Beyond ORF(3')
28071	C	T	Beyond ORF(3')
28096	C	G	Beyond ORF(3')
28403	A	G	Beyond ORF(3')
28467	C	G	Beyond ORF(3')

Context:

DNA

Position

206 GCTCAAGATTGCACAGCTGGTGAGTGGTACACTGGGACTGGAACCCAAGTGTGCCCTTAC
 TCCAGAGCCTTGGCATGCACCTGAAACCCATGTAAGCCCAGTGTGGAGACGCGCACCT
 CGAAATAATGGAATCCACTACATCAGTCCTTAGCTTCTGTGTAATCAGAGTAGCTAG
 CAGGCTCGGGATTCGCCCGGGC
 [-, T]
 TTTTTTTTTTTTTTTTTGAGACAGAGTTTGCTTTGCTTGCAGGCTGGAGTGCAAT
 GGCGCAATCTGGCTCACCGAACCTTCGCTCTCAGGTTCAAGCAATTCTCCTGCCTCA
 GCCTCCCGAGTAGCTGGATTACAGGCACCGCCACCAGGCCAGCTAATTTTTATAT
 TTTTAGTAGAGATGGGTTTACCATGTTGCCAGGCTGGCTTGAACCTTCCCCCTCTT
 ATTATAATTCAAGACACTAACCTGAAATATAACCTTTCAATGAAGTAATGGGCTTACC

(SEQ ID

NO:14)

4963 TATTAAGGGACTGGGATTCTCCCTTATCTGGCGTGTTCAGCATTAACTAAA
 TAAAGGAAAGAGTGGATGGTCAAGAAAAGCTTTCTTAAGTGATATGGACAGTTCT
 CAAGGAGGTAGAAGGGCAGCCAGGAGACAATCAAGGAGCCAACGAAATGAGTGCCTACC
 AAGTCATAGTCATTGCTTATTTAAAAATGCGTGTCTGTATGCCAGGCTCTGCACT
 GAGACCGAGAGATTCAAGATGAATAATACCTACAGTCAGTGTCTCAAATTGTGCATTA
 [C, T]
 CTAAAACACATTACATGACCATGCTGCCACTGATCGAGGCACCTTCCCAGGGCTTT
 TTTGTGAATTAAGAAAACAAGGTAATTCCAGTTATTGCCAAGATAGTTGGCTTCTTG
 GCTCATGGATATCACCTAGGCCAGTACTTTGTGATTACTGTGACTCCACTTTAAC
 GGCCTGCGATCTCTAGAGAAGAACCGCCAGGGAGCAGTGAGAGGCCCTGGTAGAC
 TGAGACACTGACTGTCCTCCCCCTATCCTTTCTGTCTTCTGCCAGCAGACCAGCAGG

(SEQ ID

NO:15)

8175 ATGCCAGGTGCCATGCTAACAGATTTGGGACACAGTGGTACCAAAACAGACAGAACCAA

FIGURE 3K



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GGAGCTGGCTTACATTCCAAGGGAGTGCATAGGAAGCTGTGTTCATTCAGTTCTGCT
CTAGTACCCCCCTTCCCTGGCAGTGCAGGGTCTGAGAAGGAAGAGTGAGGTGGAGG
AGGTGTGAAGCAGTGGGTGACCTGAGAGGAGGGATGGGTTGGCTTGCCTCAAGGCTT
GGGCCCTGCTAGGTGTCGCTCGCCTCAGGCTCTGTTCTCCCTGACACAGGCACA
[G, A]
ACTCGGCCTCCCACCCCTCCCCAAGGACATGACCTTGGGAAGGAACATATCTGAAGGCC
GCGGAGGGTTCCGCTGCTGTGCATCTGCCCCACAGATCCGAGATGCACCCACAGCTGG
GAGCACCGTTCCCTCCGCCACTGCACCTCCCTGGTTCTGTTCTCCCTCCCTCC
TCCTCTCCCCGCTCCCCAGACAGGCTGGTGTAGAGCTTATAACATGAAAGCTGATATT
TGGCATTATCCTTACCCCTGATTGCCAGCTCTCAGAGTGCCTCTGTAATCC (SEQ ID
NO:16)

10515 CTGGTGAAGGCTTGAAGAGGAAGTGACATTGAGTGGAGTCTTGAAGACTAGGCAGGAT
TCTCCAGGGGCCCTGGGTGTGGGAAAGCACACATCCTCCCTGCTAGGAGGTGCTGTG
GAGAACACCTCCAGTGGGCTGCTACTCTTCAGCCTGCTGGGCCAGCTGGAGTGGCCA
CACCATGGTCACACCAGCTGAAGTTCAAGAACGCCCTTGCAGGAGATIGCTTGTGG
TCTGGGTGAGGGCAGGTGCATCTGGAAGCCCCCTTCTTCTAAGATGTTGCTCCTGAGT
[T, C]
TCTATGTCTTAGTCTTCTTCTTCTGCTAACCTTTGCTACAGTCAGCACAGCCCTGCTG
AGAAGGAGGCTGGAGGAGTGAGTGGTCAGTAGCCTGGTGGCTTGGCTGCCCTGTGGT
GCCGCTGCCCTAACGTAGCAGGCTTAGGGAGGCAGACCCAGTCCAGGGCTGCCAATG
GGGAGCAGATGGGGTGGCTGGACACTGCACATGTCAACCAAGGCTCTAGGGAGGTCT
GTGCACAAGGCAAGTGGAAAAGCAAGGGAAAGACCCAGCCTGGTCAACATGGTAAACCC (SEQ ID
NO:17)

13034 AGATTTGGGTGAGGACACAGCCAAACCATATCAGCTCCGGATCCCTGTGTGAATGGGG
TCTTTTTGGTTGTTGAGGGCTGCACAGGGTGCACCTCTTAGAGGTGACCTCTGCCACA
ACCCACAGGAGGTGCACATGGCCACACATGCTGGTTCTGCAGTGGAGGGCTGGGG
CACTCCTGGACCTGCTGGTAACTGGAGCTGGCTGCCCTGGGATTGGGTGTCTG
CCTTGGGTTTCAGGTGTATTAGGTTGTTCTCGTTGTGGAGTCTCATACTAATGAAAAG
[T, C]
TCAGGTGCACTGCTGGCCCTTGGCTGTGGTGATCCTGGTATAACATTGGCACCC
AGAGGCAGCCCTGTTCACTGAAGCATGCGAGCTGGCTGGCAGGCAGGCAAGCTGGC
AGCTGCCCTAACCCATGAGGTGCTGCCCGTAGTAGGCACACCCCTACCTGTGCCAGAA
TTGAGGTTGAGCCAGACTCCAGGAGCCATCTGGGCCACAGGGGGCGCATTCCTCT
TTTTGTTGAAACATTCCAGCCAAGTGCCTGGCTGGGCTTCATCTCTGTCCCACCTCTCC (SEQ ID
NO:18)

13781 CCCTGTGTTATGGGTTTACACCTTATCTCACAACTTAAAAAAAAATTCTCTGAGAAT
CCTCTGTCACCCCCACTTACAGGTGAGGAACACTGAGGCAAAGATAGGCTAACCTGGCTTC
CCCAACACCATGCAGGTAAATTAGTGATAAAGCAGGGTGGAAACAAACTTGACCTCCA
ATTGTGCTCTTAATGCCAGGACACTCTGTGCTTGGCAGCACACTCTCCATGTTCT
AGGGCTTCTAGGGAGGCAGACAGTGTGGAAAGGGGTGTTCTTAGTGTGGATGTGCC
[T, C]
GCCTGCTCTTCTGTAAGCGTCACAGCACCTCACTGCTGTACTGGGAGGCACCAAGT
TTTCCCCTGTTGCCACCCAAGCGAGCTAGCTTAGGAGTCACGTGAGTGCTGGGTGTC
TCGCCCTGCTGCATCCCTCATCTGCCCTGCCCTGGGGCTGCCAGAGGAGGGCCCTGCC
GTCTCCCAGTTCTCCACAGCAGCGCTGTCCCAGCACCTGCCAGTTGTGGCCT
GGCAGCTGCTGGGCCAGACACCATACAGACAGAGTCACAGCAGGAAGAGGATGGGGCCA (SEQ ID
NO:19)

14050 GGAAGGGGTGTTCTTAGTGTGGATGTGCCCTGCCCTGCTCCTTCTGTAAGCGTCACAGC
ACCTCCACTGCTGTACTGGGAGGCACCAAGTTTCTGTTGCCACCCAAAGGCGAG
CTAGCTTAGGAGTCACGTGAGTGCTGGTGTCTGCCCTGCTGCATCCCTATCTGCC
CTGCCCTGGCTGCCAGAGGAGGGCCCTGCCAGTTCTCCAGTTCTCCACAGCAGCGCT
GTCCCAGCACCTGCCAGTTGTGGCCTGGCAGCTGCTGGGAGACACCCATACAG
[A, C]
CAGAGTCACAGCAGGAAGAGGATGGGCCAGGGCTGCTGCCCTAGGCCATGGCTGCATG
GCACCATCAGTTGATTGAGGAGCTTCTGCCAATGTCTGAGGCATCAGGTGGCAGGAC
ACGTCTCCCTGCTCTTAAGCCTCAGGCATGCAGCCCTTATGCTCTGGGGTGAAGGG

FIGURE 3L



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NO: 20)

14273

GGAGATCCCCCTCATGGAATTGCTTTTTTTTTTTTGAGACAGGGTCC
GCTCTGTCACTCAGGCTGGAGTGCAGCCTAACCTCCCAGACTCAAGTGATCCTCCTGCC

(SEQ ID

TCTCCAACAGCAGCGCTGTCCCAGCACCCCTCGGGCTCCAGTTGTGGCCTGGCAGCTGCTG
GGGCAGACACCATAACAGACAGAGTCACAGCAGGAAGAGGATGGGGCCAGGGCTGCTGCC
TCAGGCCATGGCTGCATGGCACCATCAGTTGATTGAGGAGCTTTCTGCCAATGTCTGA
GGCATCAGGTGGCAGGACACGTCTCCCTGCTTAAGCCTCAGGCATGCAGCCCTCTTA
TGCTCTCTGGGGTGAGGGGAGATCCCCCTCATGGAATTGCTTTTTTTTTTTTTTT
[-, T]
TTTTGAGACAGGGTCTGCTCTGCACTCAGGCTGGAGTGCAGCCTAACCTCCCAGACT
CAAGTGATCCTCCTGCCCTAGCCTCCGAGTAGCTGGGACCACAGGTGGACACCACACA
CCTGGGTTTTTTGTTTTGTTTTCTAGAGATGGGTCTCACTTCTGCTC
AGTCTGGTCTGAACCTCTGGGCGAAGCAGTCCTCCACCTCGTCTCCCAAAGTGT
GGATTACAGGTGTGAGGCCACTGTGCTTGGCTTTTATTATTAGAATTGTTGGAA

(SEQ ID

NO: 21)

17582

GGATGTTCTCCATGACATATATAGCTCTGAAACTACTTCTATCTAAATACACCCACA
GTGCTGTTAAAATACAGATTCTGGGCCTCACCCCTCAATTATGATTCACTGGTCTAG
GCACGTCAAGGTATTGTTCTTGTCTTAACTCAGGTCAGGTTGATTCTAAAGCCG
AAGCTCTGAAAGCACACCTTGAGAAACAGAGAACTCTTGCTCTCGCTCTTGACAC
TTCAGGTGAAAACCTTTGCTCTAATGTCGTTCTCAAACCTACGCATGTGAGAACAC
[T, C]
GTGAGAGCTTATTGAAACTGATTGGGGACCCCATACTAGAGGGCTGATTCTATAGGT
CTGAGGTAAAGCCAAGAATTGCTATTTGCTATTGCTTTCTTTCTTTCTTTCTT
TTTTTTTTTTTGAGATGAAGTCTCACCTGCCCCAGACTGGAGTGCAGTGGCATGA
TCTCAGCTACTGCAGCCTCTGCCCTGGTTAAAGCGATTCTCCACACCCAGACC
CGCTCCTGAGTAGCTGGATTACAGGTGCCACCAGTACTAGCTAACGTTGATT
TTT

(SEQ ID

NO: 22)

17700

AGGCACGTCAAGGTATTGTTCTGCTTGTAAAGTCACCCCAGGTGATTCTAAAGC
CGAAGCTCTGCAAAGCACACCTTGAGAAACAGAGAACTCTTGCTCTCGCTCTTGAC
ACTTCAGGTGAAAACCTTGCTTAATGTCGTTCTCAAACCTACGCATGTGAGAAC
ACTGTGAGAGCTTATTGAAACTGATTGGGGACCCCATACTAGAGGGCTGATTCTATA
GGTCTGAGGTAAAGCCAAGAATTGCTATTGCTATTGCTTTCTTTCTTTCTTT
[C, T]
TTTTTTTTTTTGAGATGAAGTCTCACCTGCCCCAGACTGGAGTGCAGTGGCAT
GATCTCAGCTCACTGCAGCCTCTGCCCTGGTTAAAGCGATTCTCCCACACCCAGA
CCCGCTCTGAGTAGCTGGATTACAGGTGCCACCAGTACTAGCTAACGTTGAT
TTTAGTAGAGACGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACCTGACCTCA
GGTGTACTCACCTCAGCCTCCAAAGGTCTGGGATTACTGGTGTGAGCCACCGCGTG

(SEQ ID

NO: 23)

18074

TGCAGCCTCTGCCCTGGTTAAAGCGATTCTCCCCACACCCAGACCCGCTCTGAGT
AGCTGGGATTACAGGTGCCGCCACCATGACTAGCTAACGTTGATTAGAGAC
GGGGGTTTACCATGTTGCCAGGCTGGCTCAAACCTCAGGTGATCCACTCA
CCTCAGCCTCCCAAGGTCTGGGATTACTGGTGTGAGCCACCGCGTGGGCCAGAATTG
CATTTCTAACAAAGTCCAGGTGATGTCGTTGAGGCTGGGACACACTTGAGAAC
[T, C, A]
GCTTGTACTCAGGCATATGTTGAGCAGTAGCGTCATCTCACCTGGAGCTTCTGCAG
CATCTCAGGCCTGCCCTACACCTACCGAGATCAGAATCTGCTTAACTCAATCCCGC
GTGATTCTCATGCACCTGGAAGTTGAGAAATATGACCTAGAGGAGCCGAATGT
CCACTGGAGGCAGAGATAGATGGAGAAATCTCTCTCACGGATACTAAAGATGCAA
AAAAAGGGCTGACTCTGGGTGTCAGCCAGGTGGGCTGATGACCGAAAAGAGGCCA

(SEQ ID

NO: 24)

19328

TGTGTGTGAGGCCGGGGAGTGCCTGCGAGCCCCGAATTCTCAGCCTAGTCCCCGCCA
CATAGCTAAGAAGTGAAGGAGGGAGGTGAGAAGGAGTCAGTCCCAGCCTCACTCCGGTG
GAGTACCCCTGTCCTCTGTCAGTTCAGTCTCTGGGGACAGTTGCCCTGCTTCA
CTCCATCCCTCTCTCACAGGAAAAATTACACCTTAATATTGGAAGTTCCCTCCCTA

FIGURE 3M



Docket No.: CL001188

Serial No.: 09/817,198

Inventors: YE, Jane et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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GCAAAAGTCCTTCTCAGGCACCCACAGGCAAAAAGGAAACTAAGCAGAGTTAGGGCTTCCA
[G, T]
GCCTAGCCA ACTACACGACTCTCCTTGTGCTTCCCTAAGAACCGAGCGCAAGGGGAGCGT
GGGTTCCAGCATAGATGGACCTGTGTTGGAATCTCTGCACGTGCTGTGCTGACCCCTGGCT
AGCCATTGACCTCTCTGAGCCCTTGTTCCTTCCACTAGGCTCTGTGAGGGCAGGGGCC
ATGTCTTTCACTGCTCTGTGACTGAGCACTGTGAGGGCACATAGGAAGTTCCA
TAAATGTTGTGGATAAAGGAAATAAAACCTCTCTCTCCGTCCCCCTGTGATGGC

(SEQ ID)

NO : 25)

19570 AAAGTCCTTCTCAGGCACCCACAGGCAAAAAGGAAACTAAGCAGAGTTAGGGCTTCCA
GCTAGCCA ACTACACGACTCTCCTTGTGCTTCCCTAAGAACCGAGCGCAAGGGGAGCGT
GGGTTCCAGCATAGATGGACCTGTGTTGGAATCTCTGCACGTGCTGTGCTGACCCCTGGCT
GCCATTGACCTCTCTGAGCCCTTGTTCCTTCCACTAGGCTCTGTGAGGGCAGGGGCC
TGTCTTTCACTGCTCTGTGACTGAGCACTGTGAGGGCACATAGGAAGTTCCA
[A, G]
AATGTTGTGGATAAAGGAAATAAAACCTCTCTCTCTGTCCCCCTGTGATGGC
TGCACAAGGC ACTGTGCTTGGCCAGGTTGCTAGGCTAGTGTGAGGATAAAACCAGGTATA
TTACAAATTGGAGAAAATTCTCGTTCTGTGAGAAGGTGCTGTATCATGAAACAAG
AATGTCTTGATTCCCTCATGCCAGGTA CTGGGGAGAAACAGGTGCTGATAACCGTTG
ATCCAGGCAGAAATAAGCATACTCCTGCTTCCAAGGCCGTGATGCTTCTCCTCC
(SEQ ID)

NO : 26)

20892 CCTTGGATGAAGAACGGTGGGAACTCTTGTCTTCCCTCCCGCAGTGACATGCCAT
GCCATGCCACTGCCCTTCATCTGGCTTATGACAGTCACTCATAACGACCCGATGTAC
CCGGCCCTGCACTAGCTCATGACAGCTGAGTCATGGCCAGGTGCTGTATCTCATCC
GGCCTCCTCAGCAACCCCTGAGATACTGGTAATGTCCCTGATGAAGATATTACTGAGG
CAGAAATGGACGCTCAGTGAAGCAAGGTGCTGATGTTAGCAATGAGCTATGAGTGGC
[C, T]
AGAGGGAGGAGATAAGCTCAGGCCCTGACACCAAAGCCATGCTCTTAGTCACCAC
GTGCCCTCATGGTGAATGAGTCAGCAACCAAGACGCATGAGGCCCTTTGGT
GAGCCTGGCTGGGTGCTGAGGCTTCAGGTACAATCATGGGTTGAAAGAGCCCTCCTCTC
TCTCCACAGTCTGGCACTATGACCCCTCTGGTTATTACAAGGCAAAGAGAGAGAGGAA
AGAAAGCAGGCAAATAATGTGGGTTGCTATTCTAGAGATTAGAATTTCAGGAAGGATAA
(SEQ ID)

NO : 27)

26465 TTCTCTGACCCCTCCCCCTCCGGTGCCTTCGTATCAAAGCTCCTCAAACCCCGTCCCCG
TGTGTCCTGCTGTGCGAGCTCGCTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CCCAGGCTCGTGGGGAGGTTCCACCCCTGGATCCAGGAAGAACCCCTCCACCCCTGCC
GGGTGGGCAAAGGCTACAGGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
TGCCATGGCCTGCCCTCCCCAGTGACCTGCGAAAGTGGAGCATGAGGTAGGAGGGAAAC
[G, A]
GCAACCAGGGAGTCCTCGAGCCTGGGCTGCCCTACCTTACCCATTCCCCGACCAGAGC
TTTGCCCTGCTGGCTGCCCTGCCCTTTGGGAACCTGAGCTCAGAGGCAGGTGCT
TCAGAGAAGGAAACAAATGAGGGTGGCAGGGATAAAAGTCACCTCCATTCTCTACCT
CCCCATGCAGCATGAACACAATTCTCTCCACCTGGCTCCAAATTAAAGATGTGGACCA
AGGCCTGTGGGTACTCCAGGGGCAAGGAGAGCCCTGGGTGAGTGAACACTGTCA
(SEQ ID)

NO : 28)

26472 ACCCCTCCCCCTCCGGTGCCTTCGTATCAAAGCTCCTCAAACCCCGTCCCCCGTGT
TGCTGTGCGAGCTCGCTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
TCGTGGGGAGGTTCCACCCCTGGATCCAGGAAGAACCCCTCCACCCCTGCC
CCAAAGGCTACAGGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
GGCCTGCCCTCCCCAGTGACCTGCGAAAGTGGAGCATGAGGTAGGAGGGAAACGGCA
[A, G]
GGGAGTCCTCGAGCCTGGGCTGCCCTACCTTACCCATTCCCCGACCAGAGCTTGCCC
TTGCTTGGCTGCCCTGCCCTTTGGGAACCTGAGCTCAGAGGCAGGTGCTTCAGAGA
AGGAAACAAATGAGGGTGGCAGGGATAAAAGTCACCTCCATTCTCTACCTCC
AGCATGAACACAATTCTCTCCACCTGGCTCCAAATTAAAGATGTGGACCAAGGGCTG
TGGGTACTCCAGGGGCAAGGAGAGCCCTGGGTGAGTGAACACTGTCA
(SEQ ID)

NO : 29)

FIGURE 3N



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Docket No.: CL001188
 Serial No.: 09/817,198
 Inventors: YE, Jane et al.
 Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

28071

GCCAGGGACTTGAGAAGTTATGGGCACTGGCTCCAATCTGTGGACCAGTATTCAGC
 TTTCCCTGAAGATCAGGCAGGGTGCATTCTTCTCTCTAGCCCCCTCAGGAA
 AGAAGGACTATATTTGACTGTACCCCTAGGGTCTGGAAGGGAAAACATGGAATCAGGA
 TTCTATAGACTGATAGGCCCTATCCACAAGGCCATGACTGGGAAAAGGTATGGGAGCAG
 AAGGAGAATTGGGATTTAGGGTCAGCTACCGCTCACCTAAACCTTGGTGGCCTGGGG
 [C, T]
 ATGTCTTGAGGCCAGACTGTTAACCAAGGCTCTGCTGGCTGTTACTCGTCACCCACCTC
 TGCACTGCTGCTTGAGACTCCATCCAGCCCAGGCACGCCACTGCTCTGAGCCTCC
 ACTATCTCCCTGTGACGGGTGAACTTCGTGACTGTGTCGGTCCATATATGAATTGT
 GAGCAGGGTCATCTATTTAAACACAGATGTTACAAATAAGATTATTCACACAC
 CGGTGTGGCTGCCTGGATGAGTCCTGGGGTAGGTCTACTCAGACCCGGCAGTGATG
 (SEQ ID)

NO: 30)

28096

GGCAGTGGCTCCAATCTGTGGACCAGTATTCAGCTTCCCTGAAGATCAGGCAGGGTGC
 CATTCAATTGCTTTCTCTCCCTAGCCCCCTCAGGAAAGAAGGACTATATTTGACTGTACC
 CTAGGGTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTATCC
 ACAAGGGCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTAGGGTGC
 AGCTACGCTCACCCCTAAACCTTGGTGGCCTGGGATGCTTGAGGCCAGACTGTTAA
 [C, G]
 CAGGCTCTGCTGGCCTGTTACTCGTACCCACTCTGCACCTGCTGCTTGAGACTCCAT
 CCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACT
 TC GTGACTGTGTCGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTAAACA
 CAGATGTTACAAAATAAGATTATTCACACCCACCGGTGTTGGCTGCCCTGGATGAGTCCT
 TGGGGTAGGTCTACTCAGACCCGGCAGTGATGTTGGGAGAGAGGCACTGCTGGT
 (SEQ ID)

NO: 31)

28403

CTGCTGGCCTGTTACTCGTACCCACTCTGCACCTGCTGCTTGAGACTCCATCCAGCC
 CCAGGCAGGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGT
 ACTGTGTCGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTAAACACAGATG
 TTTACAAAATAAGATTATTCACACCCACCGGTGTTGGCTGCCCTGGATGAGTCCTGGGG
 TAGGTCTCACTCAGACCCCTGGCAGTGATGTTGGGAGAGAGGCACTGCTGGTACAAGC
 [A, G]
 GCTCCAGAAGCAAAGGCAACAGCAGTAGAGTGACCAACGGAAAGCGGAAACATTGTCTTCC
 CTTCTCTACCTTCCCTAGTGCACCTGCAGGGAGGCCAAAGCAAAGCCCCGTTGCCCTG
 CATTGGGCTGGCACTGCAGAAATAAGATGAAACACAGTTATCGAGAGGGATGCTGAACATC
 TATGAGCAGGTTAAAGCCAAGATGAGTCATCTGTTGTGTTGGCTAGGAACGGGTC
 TTCCTGAAGGCATGAGGTGGACTGGATAATCTTCAGATTGTGATTGGATAACCTCGGG
 (SEQ ID)

NO: 32)

28467

GCACGCCACCTGCTCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTACTG
 TGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTAAACACAGATGTTA
 CAAAATAAGATTATTCACACCCACCGGTGTTGGCTGCCCTGGATGAGTCCTGGGGTAGG
 TCTCACTCAGACCCCTGGCAGTGATGTTGGGAGAGAGGCACTGCTGGTACAAGCAGCT
 CCAGAAGCAAAGGCAACAGCAGTAGAGTGACCAACGGAAAGCGGCAAACATTGTCTCC
 [C, G]
 TCTACCTTCCCTAGTGCACCTGCAGGGAGGCCAAAGCAAAGCCCCGTTGCCCTGCATT
 GGGCTGGCACTGCAGAAATAAGATGAAACACAGTTATCGAGAGGGATGCTGAACATCTATG
 AGCAGGTTAAAGCCAAGATGAGTCATCTGTTGTGTTGGCTAGGAACGGGCTTCC
 TGAAGGCATGAGGTGGACTGGATAATCTTCAGATTGTGATTGGATAACCTCGGGGAG
 CAGAGGCAGACTGGGATCTCAGGACTGCAGGTATTCATACTTGGGATATGAAATTGAT
 (SEQ ID)

NO: 33)

FIGURE 30